

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2003, 23:56:24 ; Search time 8 Seconds
(without alignments)
1027.619 Million cell updates/sec

Title: US-09-877-633-2

Perfect score: 2028

Sequence: 1 caaaaggcaagataataaa.....agtagacagtgatgga 2028

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 5275 seqs, 2026861 residues

Total number of hits satisfying chosen parameters: 10550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 350 summaries

Database :

Caenorhab

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estnu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_estfun.*

9: em_estom.*

10: em_hic.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	35.6	1.8	308	9	Bi404900 MI-P-NA-a
C 2	35.2	1.7	659	3	Au212636 Caenorhab
C 3	32.6	1.6	195	9	Bf713200 MI-P-O2-a
C 4	32.2	1.6	465	9	Bi400626 MI-P-AY1-
C 5	31.4	1.5	259	9	Bf702228 MI-P-A2-a
C 6	31.4	1.5	500	2	Bm740200 K-EST0011
C 7	31.4	1.5	556	9	Bf702953 MI-P-H1-a
C 8	31.2	1.5	136	2	HS0010501
C 9	31.2	1.5	374	9	Bf712847 MI-P-O1-a
C 10	31	1.5	472	2	HS0002682
C 11	30.8	1.5	400	9	Bf712218 Homo sapi
C 12	30.6	1.5	502	9	Bf703505 MI-P-H1-a
C 13	30.2	1.5	321	6	BQ236337 TAE05035A
C 14	30.2	1.5	512	9	Bf713152 MI-P-O1-a
C 15	30	1.5	273	2	HS0002678
C 16	29.8	1.5	300	9	Bf711870 MI-P-O3-a
C 17	29.6	1.5	127	2	HS0010205
C 18	29.4	1.4	147	2	HS0003359
C 19	29.4	1.4	150	9	Bf711427 MI-P-A2-a
C 20	29.4	1.4	414	9	Bf712867 MI-P-O1-a
C 21	29.4	1.4	417	9	Bf704037 MI-P-A3-a
C 22	29.2	1.4	144	2	HS0001232
C 23	29.2	1.4	206	9	Bf713586 MI-P-O2-a

C 24	29.2	1.4	306	9	Bi404658
C 25	29.2	1.4	385	9	Bf703246
C 26	29.2	1.4	422	6	Bm377646 EBem04 SQ
C 27	29.2	1.4	445	9	Bf711499 MI-P-A2-a
C 28	29	1.4	311	9	Bf702714 MI-P-E3-a
C 29	29	1.4	412	9	Bf713046 MI-P-H3-a
C 30	29	1.4	428	9	Bf704356 MI-P-O3-a
C 31	29	1.4	576	9	Bi400750 MI-P-AY1-
C 32	28.8	1.4	130	2	HS0005765
C 33	28.8	1.4	137	2	HS0002748
C 34	28.8	1.4	197	9	Bf709714 MI-P-AV1-
C 35	28.8	1.4	313	9	Bf709877 MI-P-AV1-
C 36	28.6	1.4	115	2	HS0010170
C 37	28.6	1.4	277	2	HS0004384
C 38	28.6	1.4	288	9	Bf703566 MI-P-H1-a
C 39	28.6	1.4	391	9	Bf704175 MI-P-O3-a
C 40	28.4	1.4	112	2	HS0001422
C 41	28.4	1.4	245	9	Bf703358
C 42	28.4	1.4	273	9	Bf708447 MI-P-AV0-
C 43	28.4	1.4	422	6	Bm377646
C 44	28.2	1.4	129	2	HS0011693
C 45	28	1.4	131	2	HS0010495
C 46	28	1.4	308	9	Bf713343
C 47	28	1.4	331	6	Bm444148
C 48	28	1.4	348	3	AU209841
C 49	28	1.4	498	2	Bm832939
C 50	28	1.4	522	9	Bf713161
C 51	27.8	1.4	337	9	Bf702115
C 52	27.8	1.4	343	2	HSC9743
C 53	27.8	1.4	460	6	BM099974
C 54	27.8	1.4	716	3	AU217241
C 55	27.6	1.4	124	2	HS0010444
C 56	27.6	1.4	284	9	Bf703336
C 57	27.6	1.4	348	2	HS0002737
C 58	27.6	1.4	444	6	Bm378023
C 59	27.6	1.4	522	9	Bi400734
C 60	27.6	1.4	569	2	Bm818575
C 61	27.6	1.4	647	2	HS0012004
C 62	27.6	1.4	798	2	HS0003964
C 63	27.4	1.4	125	2	HS0001209
C 64	27.4	1.4	142	2	HS0003075
C 65	27.4	1.4	380	9	Bf711490
C 66	27.4	1.4	402	6	Bm372823
C 67	27.4	1.4	437	6	Bm370203
C 68	27.4	1.4	604	2	Bm854730
C 69	27.4	1.4	680	2	HS0002724
C 70	27.2	1.3	269	9	Bf703694
C 71	27.2	1.3	382	2	HSC2714
C 72	27.2	1.3	571	3	AU218039
C 73	27	1.3	125	2	HS0010819
C 74	27	1.3	265	2	HS0002746
C 75	27	1.3	649	9	Bf703011
C 76	26.8	1.3	120	2	HS0010864
C 77	26.8	1.3	128	2	HS0010497
C 78	26.8	1.3	139	2	HS0001338
C 79	26.8	1.3	147	2	HS0002744
C 80	26.8	1.3	224	9	Bf703629
C 81	26.8	1.3	361	2	HS0003968
C 82	26.8	1.3	445	9	Bi400057
C 83	26.8	1.3	454	2	HS0011933
C 84	26.8	1.3	469	9	Bf711270
C 85	26.8	1.3	498	2	Bm856410
C 86	26.6	1.3	110	2	HS0004754
C 87	26.6	1.3	124	9	Bf702532
C 88	26.6	1.3	127	2	HS0010835
C 89	26.6	1.3	217	9	Bf703980
C 90	26.6	1.3	240	9	Bf713193
C 91	26.6	1.3	300	9	Bf709445
C 92	26.6	1.3	346	9	Bf710556
C 93	26.6	1.3	352	9	Bf711589
C 94	26.6	1.3	366	9	Bf711564
C 95	26.6	1.3	443	6	Bm374465
C 96	26.6	1.3	446	9	Bf702796

Bi404658	MI-P-NA-a
Bf703246	MI-P-O2-a
Bm377646	EBem04 SQ
Bf711499	MI-P-A2-a
Bf702714	MI-P-E3-a
Bf713046	MI-P-H3-a
Bf704356	MI-P-O3-a
Bi400750	MI-P-AY1-
Al041289	Homo sapi
Al038402	Homo sapi
Bf709714	MI-P-AV1-
Bf709877	MI-P-AV1-
Al045320	Homo sapi
Al039908	Homo sapi
Bf703566	MI-P-H1-a
Al04175	MI-P-O3-a
Al037097	Homo sapi
Bf703358	MI-P-O3-a
Bf708447	MI-P-AV0-
Bm377646	EBem04 SQ
Al046843	Homo sapi
Al045645	Homo sapi
Bf713343	MI-P-O2-a
Bm444148	EBem09 SQ
Au209841	Caenorhab
Bm832939	K-EST0107
Bf713161	MI-P-O1-a
Bf702115	MI-P-A1-a
C03974	Human Heart
Bm099974	EBes01 SQ
Au217241	Caenorhab
Al045594	Homo sapi
Bf703336	MI-P-A3-a
Al038391	Homo sapi
Bm378023	EBem04 SQ
Bi400734	MI-P-AV1-
Bm818575	K-EST0085
Al041754	Homo sapi
Al036892	Homo sapi
Al038599	Homo sapi
Al038599	Homo sapi
Bf711490	MI-P-O3-a
Bm372823	EBma04 SQ
Bm370203	EBro08 SQ
Bm854730	K-EST0137
Al038379	Homo sapi
Bf703694	MI-P-E4-a
C04271	Human Heart
Au218039	Caenorhab
Al045969	Homo sapi
Al038400	Homo sapi
Bf703011	MI-P-E5-a
Al046014	Homo sapi
Al045647	Homo sapi
Al037014	Homo sapi
Al038398	Homo sapi
Bf703629	MI-P-H1-a
Al039492	Homo sapi
Bi400057	MI-P-AV1-
Al047083	Homo sapi
Al041270	MI-P-O3-a
Bm856410	K-EST0140
Al040278	Homo sapi
Bf702532	MI-P-E3-a
Al045985	Homo sapi
Bf703980	MI-P-O1-a
Bf713193	MI-P-O1-a
Bf710556	MI-P-AV1-
Bf711589	MI-P-A1-a
Bf711564	MI-P-A2-a
Bm374465	EBp103 SQ
Bf702796	MI-P-H3-a

97	26.6	1.3	451	2	HSM004354	Al039878 Homo sapi	C 170	25.2	1.2	409	2	BM856839	BM856839 K-EST0140
98	26.6	1.3	485	2	BM856662	BM856662 K-EST0140	C 171	25.2	1.2	431	9	BF703269	BF703269 MI-P-A3-a
99	26.6	1.3	609	2	HSM002666	Al038323 Homo sapi	C 172	25.2	1.2	451	9	BF702085	BF702085 MI-P-A1-a
100	26.6	1.3	672	2	BM851675	BM851675 K-EST0132	C 173	25.2	1.2	453	2	AF120351	AF120351 Homo sapi
101	26.4	1.3	114	2	HSM010848	Al045998 Homo sapi	C 174	25.2	1.2	582	2	BF738713	BF738713 K-EST0006
102	26.4	1.3	129	2	HSM005730	Al041254 Homo sapi	C 175	25.2	1.2	597	6	BM374584	BM374584 EBma05 SQ
103	26.4	1.3	288	9	BF703718	BF703718 MI-P-E4-a	C 176	25.2	1.2	632	3	AU217172	AU217172 Caenorhab
104	26.4	1.3	351	9	BF710483	BF710483 MI-P-A1-a	C 177	25	1.2	64	2	HSM002423	Al038084 Homo sapi
105	26.4	1.3	439	2	AF119319	AF119319 Homo sapi	C 178	25	1.2	84	2	HSM002938	Al038462 Homo sapi
106	26.4	1.3	446	2	BM830489	BM830489 K-EST0104	C 179	25	1.2	118	2	HSM002462	Al038123 Homo sapi
107	26.4	1.3	454	2	AF119566	AF119566 Homo sapi	C 180	25	1.2	138	9	BF709622	BF709622 MI-P-A1-a
108	26.4	1.3	536	9	BF713165	BF713165 MI-P-O1-a	C 181	25	1.2	151	2	HSM002734	Al038388 Homo sapi
109	26.4	1.3	682	3	AU216796	AU216796 Caenorhab	C 182	25	1.2	270	9	BF702005	BF702005 MI-P-A1-a
110	26.2	1.3	156	2	HSM002751	Al038405 Homo sapi	C 183	25	1.2	272	9	BI400234	BI400234 MI-P-A1-a
111	26.2	1.3	233	9	BI400101	BI400101 MI-P-A1-a	C 184	25	1.2	296	9	BI400524	BI400524 MI-P-A1-a
112	26.2	1.3	311	9	BI400269	BI400269 MI-P-A1-a	C 185	25	1.2	372	9	BI400593	BI400593 MI-P-A1-a
113	26.2	1.3	377	9	BF712991	BF712991 MI-P-O2-a	C 186	25	1.2	381	2	BM823395	BM823395 K-EST0094
114	26.2	1.3	448	9	BF702426	BF702426 MI-P-A2-a	C 187	25	1.2	389	9	BF712307	BF712307 MI-P-A3-a
115	26.2	1.3	498	2	BM856410	BM856410 K-EST0140	C 188	25	1.2	400	6	BQ241093	BQ241093 TAE05009C
116	26.2	1.3	512	6	BQ236750	BQ236750 TAE05027D	C 189	25	1.2	420	6	BQ250523	BQ250523 TAE25003G
117	26.2	1.3	573	9	BF702348	BF702348 MI-P-A2-a	C 190	25	1.2	426	9	BF703733	BF703733 MI-P-E4-a
118	26	1.3	124	2	HSM010174	Al045324 Homo sapi	C 191	25	1.2	428	9	BF703873	BF703873 MI-P-O1-a
119	26	1.3	139	2	HSM0011341	Al037017 Homo sapi	C 192	25	1.2	452	9	BF702324	BF702324 MI-P-A2-a
120	26	1.3	144	2	HSM0011210	Al036893 Homo sapi	C 193	25	1.2	652	2	HSM035653	BM835653 K-EST0110
121	26	1.3	230	6	BM445013	BM445013 EBem09 SQ	C 194	24.8	1.2	61	2	HSM011387	Al038352 Homo sapi
122	26	1.3	270	9	BF702005	BF702005 MI-P-A1-a	C 195	24.8	1.2	102	2	HSM011387	Al046537 Homo sapi
123	26	1.3	366	9	BF712209	BF712209 MI-P-E4-a	C 196	24.8	1.2	110	2	HSM010681	Al045831 Homo sapi
124	26	1.3	423	9	BI404717	BI404717 MI-P-NA-a	C 197	24.8	1.2	118	9	BF703409	BF703409 MI-P-O3-a
125	26	1.3	438	2	BM853947	BM853947 K-EST0136	C 198	24.8	1.2	133	2	HSM004867	Al040391 Homo sapi
126	26	1.3	451	2	AF120342	AF120342 Homo sapi	C 199	24.8	1.2	255	2	AF119299	AF119299 Homo sapi
127	26	1.3	550	2	BM850577	BM850577 K-EST0131	C 200	24.8	1.2	255	2	AF119300	AF119300 Homo sapi
128	26	1.3	572	6	BQ237294	BQ237294 TAE05019B	C 201	24.8	1.2	331	9	BF704028	BF704028 MI-P-A3-a
129	26	1.3	574	2	BM833156	BM833156 K-EST0107	C 202	24.8	1.2	351	9	BF710483	BF710483 MI-P-A1-a
130	26	1.3	603	6	BQ240324	BQ240324 TAE05019B	C 203	24.8	1.2	370	6	BM099840	BM099840 EBem01 SQ
131	26	1.3	1133	2	HSM0007179	Al042329 Homo sapi	C 204	24.8	1.2	389	6	BF778083	BF778083 EBR007 SQ
132	25.8	1.3	97	2	HSM002694	Al038350 Homo sapi	C 205	24.8	1.2	432	9	BF703444	BF703444 MI-P-H1-a
133	25.8	1.3	135	9	BF709090	BF709090 MI-P-A1-a	C 206	24.8	1.2	433	6	BM370064	BM370064 EBR008 SQ
134	25.8	1.3	233	9	BF711163	BF711163 MI-P-A1-a	C 207	24.8	1.2	439	6	BM370961	BM370961 EBR004 SQ
135	25.8	1.3	222	9	BF703778	BF703778 MI-P-E4-a	C 208	24.8	1.2	441	6	BM370961	BM370961 EBR004 SQ
136	25.8	1.3	344	9	BF702922	BF702922 MI-P-H2-a	C 209	24.8	1.2	461	6	BM097368	BM097368 EBR001 SQ
137	25.8	1.3	430	9	BF702316	BF702316 MI-P-A2-a	C 210	24.8	1.2	476	6	BM441946	BM441946 EBR001 SQ
138	25.8	1.3	441	6	BM377494	BM377494 EBem04 SQ	C 211	24.8	1.2	509	9	BI404683	BI404683 MI-P-NA-a
139	25.8	1.3	572	6	BQ236179	BQ236179 TAE05037B	C 212	24.8	1.2	515	2	BM829919	BM829919 K-EST0103
140	25.8	1.3	597	2	BM782406	BM782406 K-EST0059	C 213	24.8	1.2	535	2	BM836836	BM836836 K-EST0112
141	25.8	1.3	652	2	HSM001625	Al037299 Homo sapi	C 214	24.8	1.2	556	2	BM831327	BM831327 K-EST0107
142	25.6	1.3	145	2	HSM002494	Al038155 Homo sapi	C 215	24.8	1.2	617	2	BM827422	BM827422 K-EST0099
143	25.6	1.3	288	9	BF703566	BF703566 MI-P-H1-a	C 216	24.8	1.2	632	6	BQ238563	BQ238563 TAE05002E
144	25.6	1.3	292	6	BM443562	BM443562 EBR002 SQ	C 217	24.8	1.2	642	2	BM787544	BM787544 K-EST0110
145	25.6	1.3	356	9	BF711582	BF711582 MI-P-A1-a	C 218	24.8	1.2	705	2	BM835702	BM835702 K-EST0066
146	25.6	1.3	357	6	BM098386	BM098386 EBem08 SQ	C 219	24.6	1.2	103	2	HSM001297	Al036974 Homo sapi
147	25.6	1.3	380	9	BF713194	BF713194 MI-P-O1-a	C 220	24.6	1.2	107	2	HSM002922	Al038446 Homo sapi
148	25.6	1.3	441	6	BM369984	BM369984 EBR008 SQ	C 221	24.6	1.2	109	2	HSM001301	Al036978 Homo sapi
149	25.6	1.3	468	2	BM856544	BM856544 K-EST0140	C 222	24.6	1.2	126	2	HSM005648	Al041172 Homo sapi
150	25.6	1.3	536	5	BQ109625	BQ109625 imagec 9	C 223	24.6	1.2	133	2	HSM0003063	Al038557 Homo sapi
151	25.6	1.3	587	2	BM793473	BM793473 K-EST0074	C 224	24.6	1.2	206	9	BF709088	BF709088 MI-P-A1-a
152	25.4	1.3	93	2	HSM002749	Al038403 Homo sapi	C 225	24.6	1.2	255	2	AF119298	AF119298 Homo sapi
153	25.4	1.3	306	9	BI404658	BI404658 MI-P-NA-a	C 226	24.6	1.2	309	6	BQ240344	BQ240344 TAE05018H
154	25.4	1.3	347	6	BM101379	BM101379 EBR010 SQ	C 227	24.6	1.2	334	6	BM371424	BM371424 EBma08 SQ
155	25.4	1.3	416	9	BF712777	BF712777 MI-P-H1-a	C 228	24.6	1.2	356	9	BF713064	BF713064 MI-P-H3-a
156	25.4	1.3	426	9	BF704519	BF704519 MI-P-E3-a	C 229	24.6	1.2	416	9	BF702792	BF702792 MI-P-H3-a
157	25.4	1.3	446	9	BF701919	BF701919 MI-P-E4-a	C 230	24.6	1.2	420	2	BM752420	BM752420 K-EST0028
158	25.4	1.3	461	2	HSM002758	Al038412 Homo sapi	C 231	24.6	1.2	442	2	BM855589	BM855589 K-EST0138
159	25.4	1.3	481	6	BM441017	BM441017 EBR002 SQ	C 232	24.6	1.2	459	2	AF119565	AF119565 Homo sapi
160	25.4	1.3	484	9	BF711440	BF711440 MI-P-A2-a	C 233	24.6	1.2	490	9	BF713184	BF713184 MI-P-O1-a
161	25.4	1.3	511	9	BI400531	BI400531 MI-P-A1-a	C 234	24.6	1.2	494	3	AU217784	AU217784 Caenorhab
162	25.4	1.3	595	3	AU221564	AU221564 Caenorhab	C 235	24.6	1.2	502	9	BI400688	BI400688 MI-P-A1-a
163	25.2	1.2	74	2	HSM003089	Al038613 Homo sapi	C 236	24.6	1.2	514	3	AU217052	AU217052 Caenorhab
164	25.2	1.2	80	2	HSM003090	Al038614 Homo sapi	C 237	24.6	1.2	517	9	BF709457	BF709457 MI-P-A1-a
165	25.2	1.2	97	2	HSM001884	Al037553 Homo sapi	C 238	24.6	1.2	669	3	AU209958	AU209958 Caenorhab
166	25.2	1.2	113	2	HSM002662	Al038319 Homo sapi	C 239	24.4	1.2	90	2	HSM003105	Al038629 Homo sapi
167	25.2	1.2	190	9	BF704023	BF704023 MI-P-A3-a	C 240	24.4	1.2	110	2	HSM010752	Al045902 Homo sapi
168	25.2	1.2	245	9	BF709664	BF709664 MI-P-A1-a	C 241	24.4	1.2	123	9	BF709082	BF709082 MI-P-A1-a
169	25.2	1.2	398	9	BF702734	BF702734 MI-P-E3-a	C 242	24.4	1.2	133	2	HSM002918	Al038442 Homo sapi

243	24.4	1.2	163	9	BF713226	BF713226 MI-P-O1-a	C 316	24	1.2	447	2	AF119559	AF119559 Homo sapi
244	24.4	1.2	265	9	BF399011	BF399011 MI-P-AV1-	317	24	1.2	448	9	BF711461	BF711461 MI-P-O3-a
c 245	24.4	1.2	283	3	AU216457	Au216457 Caenorhab	318	24	1.2	453	9	BF713178	BF713178 MI-P-O1-a
246	24.4	1.2	298	9	BF401983	Bi401983 MI-P-CP0-	319	24	1.2	458	2	AF120341	AF120341 Homo sapi
247	24.4	1.2	340	9	BF710205	BF710205 MI-P-AV1-	320	24	1.2	464	2	AF120354	AF120354 Homo sapi
c 248	24.4	1.2	345	9	BF404800	Bi404800 MI-P-H5-a	c 321	24	1.2	497	9	Bi400892	Bi400892 MI-P-AV1-
249	24.4	1.2	347	9	BF709485	BF709485 MI-P-AV0-	c 322	24	1.2	511	9	Bi400531	Bi400531 MI-P-AV1-
c 250	24.4	1.2	355	9	BF704170	BF704170 MI-P-O3-a	323	24	1.2	514	6	BQ240147	BQ240147 TaEO5021E
251	24.4	1.2	358	6	BF779820	BF779820 EBem07_SQ	324	24	1.2	523	2	BM739652	BM739652 K-EST0009
c 252	24.4	1.2	375	9	BF709762	BF709762 MI-P-AV0-	325	24	1.2	563	2	BSM004571	BSM004571 Homo sapi
c 253	24.4	1.2	436	2	BM854830	BM854830 K-EST0137	c 326	24	1.2	563	9	BF711476	BF711476 MI-P-O3-a
254	24.4	1.2	438	6	BM099169	BM099169 EBem01_SQ	c 327	24	1.2	570	2	BM854872	BM854872 K-EST0137
255	24.4	1.2	441	6	BM375590	BM375590 EBem06_SQ	c 328	24	1.2	628	9	BF713187	BF713187 MI-P-O1-a
256	24.4	1.2	442	6	BM099642	BM099642 EBem01_SQ	329	23.8	1.2	70	2	BSM010676	BSM010676 Homo sapi
257	24.4	1.2	454	2	AF119566	AF119566 Homo sapi	330	23.8	1.2	91	2	BSM011994	BSM011994 Homo sapi
c 258	24.4	1.2	461	2	AF120340	AF120340 Homo sapi	331	23.8	1.2	103	2	BSM010743	BSM010743 Homo sapi
c 259	24.4	1.2	502	2	BSM004322	BSM004322 MI-P-E6-a	332	23.8	1.2	112	2	BSM011301	BSM011301 Homo sapi
c 260	24.4	1.2	506	9	BF704422	BF704422 MI-P-E6-a	c 333	23.8	1.2	119	2	BSM003284	BSM003284 Homo sapi
261	24.4	1.2	618	2	BSM53322	BSM53322 K-EST0136	c 334	23.8	1.2	134	2	BSM001164	BSM001164 Homo sapi
262	24.4	1.2	650	2	BSM27765	BSM27765 K-EST0100	335	23.8	1.2	142	2	BSM002924	BSM002924 Homo sapi
263	24.4	1.2	651	2	BSM29019	BSM29019 K-EST0101	336	23.8	1.2	167	9	BF704551	BF704551 MI-P-H4-a
264	24.2	1.2	107	2	BSM010727	BSM010727 Homo sapi	337	23.8	1.2	179	9	BF708579	BF708579 MI-P-AV0-
265	24.2	1.2	108	2	BSM003026	BSM003026 Homo sapi	338	23.8	1.2	206	9	BF713586	BF713586 MI-P-O2-a
266	24.2	1.2	122	2	BSM002679	BSM002679 Homo sapi	339	23.8	1.2	253	2	BSM002762	BSM002762 Homo sapi
268	24.2	1.2	135	2	BSM002756	BSM002756 Homo sapi	c 340	23.8	1.2	257	9	BF400793	BF400793 MI-P-AV1-
269	24.2	1.2	151	9	BF399411	BF399411 MI-P-AV1-	c 341	23.8	1.2	265	9	BF399011	BF399011 MI-P-AV1-
c 270	24.2	1.2	174	9	BF710762	BF710762 MI-P-AV1-	c 343	23.8	1.2	270	2	HSC5696	BSM004384
c 271	24.2	1.2	333	9	BF712166	BF712166 Homo sapi	c 344	23.8	1.2	277	2	BSM004384	BSM004384 Homo sapi
c 272	24.2	1.2	336	2	HSC6892	BSM004384 Homo sapi	c 345	23.8	1.2	286	9	BF713516	BF713516 MI-P-E3-a
c 273	24.2	1.2	345	9	BF702107	BF702107 MI-P-A1-a	346	23.8	1.2	307	9	BF713181	BF713181 MI-P-O1-a
c 274	24.2	1.2	368	2	HSC3975	BSM004384 Homo sapi	c 347	23.8	1.2	310	2	BSM035906	BSM035906 K-EST0111
c 275	24.2	1.2	379	2	HSC4704	BSM004384 Homo sapi	c 348	23.8	1.2	342	9	BF399743	BF399743 MI-P-AV1-
c 276	24.2	1.2	388	2	HSC4045	BSM004384 Homo sapi	c 349	23.8	1.2	354	9	BF701908	BF701908 MI-P-E3-a
c 277	24.2	1.2	393	9	BF711193	BF711193 MI-P-E6-a	350	23.8	1.2	372	6	BM369980	BM369980 EBRO08_SQ
c 278	24.2	1.2	399	6	BSM69181	BSM69181 EBRO07_SQ							
c 279	24.2	1.2	402	2	HSC7862	BSM69181 EBRO07_SQ							
c 280	24.2	1.2	416	9	BF704396	BF704396 MI-P-E6-a							
c 281	24.2	1.2	440	6	BF779326	BF779326 EBRO01_SQ							
c 282	24.2	1.2	444	6	BSM374457	BSM374457 EBPI03_SQ							
c 283	24.2	1.2	449	2	BSM000056	BSM000056 Homo sapi							
c 284	24.2	1.2	457	6	BQ236739	BQ236739 TaEO5027E							
c 285	24.2	1.2	494	2	AF119561	AF119561 Homo sapi							
c 286	24.2	1.2	503	2	BF768743	BF768743 K-EST0051							
c 287	24.2	1.2	522	2	BSM011999	BSM011999 Homo sapi							
c 288	24.2	1.2	601	2	BSM011999	BSM011999 Homo sapi							
c 289	24.2	1.2	623	3	AU212629	Au212629 Caenorhab							
c 290	24.2	1.2	665	3	AU214507	Au214507 Caenorhab							
c 291	24.2	1.2	671	6	BSM004268	BSM004268 Homo sapi							
c 292	24.2	1.2	679	2	BSM004268	BSM004268 Homo sapi							
c 293	24.2	1.2	694	3	AU218691	Au218691 Caenorhab							
c 294	24.2	1.2	753	3	AU217453	Au217453 Caenorhab							
c 295	24.2	1.2	798	2	BSM004616	BSM004616 Homo sapi							
c 296	24.2	1.2	92	2	BSM0010774	BSM0010774 Homo sapi							
c 297	24.2	1.2	102	2	BSM010480	BSM010480 Homo sapi							
c 298	24.2	1.2	153	3	AU217183	Au217183 Caenorhab							
c 299	24.2	1.2	161	9	BF711317	BF711317 MI-P-A1-a							
c 300	24.2	1.2	184	9	BF708956	BF708956 MI-P-AV0-							
c 301	24.2	1.2	196	9	BF712210	BF712210 MI-P-E4-a							
c 302	24.2	1.2	246	9	BF711496	BF711496 MI-P-A2-a							
c 303	24.2	1.2	249	6	BF777589	BF777589 EBRO04_SQ							
c 304	24.2	1.2	268	9	BF708508	BF708508 MI-P-AV0-							
c 305	24.2	1.2	270	9	BF709379	BF709379 MI-P-AV0-							
c 306	24.2	1.2	279	6	BSM371293	BSM371293 EBRO08_SQ							
c 307	24.2	1.2	315	9	BF400119	BF400119 MI-P-AV1-							
c 308	24.2	1.2	322	9	BF702047	BF702047 MI-P-A1-a							
c 309	24.2	1.2	380	2	AF121329	AF121329 Homo sapi							
c 310	24.2	1.2	385	9	BF703427	BF703427 MI-P-H1-a							
c 311	24.2	1.2	385	9	BF703704	BF703704 MI-P-E4-a							
c 312	24.2	1.2	391	9	BF704458	BF704458 MI-P-E6-a							
c 313	24.2	1.2	393	6	BF779723	BF779723 EBRO05_SQ							
c 314	24.2	1.2	415	9	BF709503	BF709503 MI-P-AV0-							
c 315	24.2	1.2	444	6	BM443476	BM443476 EBRO02_SQ							

ALIGNMENTS

RESULT 1

BI404900/c standard; RNA; EST; 308 BP.

ID BI404900 standard; RNA; EST; 308 BP.

XX BI404900;

XX BI404900.1

SV BI404900.1

DT 15-AUG-2001 (Rel. 68, Created)

DT 15-AUG-2001 (Rel. 68, Last updated, Version 1)

DE MI-P-NA-aeg-e-07-1-UM.abl MI-P-NA Sus scrofa cDNA clone

DE MI-P-NA-aeg-e-07-1-UM.abl 3', mRNA sequence.

XX EST.

XX Sus scrofa (pig)

OC Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

XX [1]

XX MEDLINE; 97044477.

XX 1-308

RA Ronaldo M.F., Lennon G., Soares M.B.

RT "Normalization and subtraction: two approaches to facilitate gene

RL discovery";

XX Genome Res. 6(9):791-806(1996).

XX UNILIB; 9699; 9699.

XX Contact: Tuggle CK

CC Molecular Genetics Laboratory, Department of Animal Science

CC Iowa State University

CC	201 Kildree Hall, Ames, IA 50011-3150, USA	
CC	Tel: 5152944252	
CC	Fax: 5152942401	
CC	Email: cktuggle@iasstate.edu	
CC	The sequence contained an oligo-dT track that was present in the	
CC	oligonucleotide that was used to prime the synthesis of first	
CC	strand cDNA and therefore this may represent a bonafide poly A	
CC	tail. The sequence tag present in the cDNA between the NotI site	
CC	and the oligo-dT track served to identify it as a clone from the	
CC	normalized anterior pituitary at estrus day 12 library cDNA Library	
CC	Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science	
CC	Research Center, Department of Animal Science, University of	
CC	Missouri-Columbia, 65211 Clone distribution: clones will be	
CC	available through Research Genetics (www.resgen.com)	
CC	Seq primer: M13 Forward	
CC	POLYA=Yes.	
XX		
XX	Key	Location/Qualifiers
PH		
FT	source	1. .308
FT		/db_xref="taxon:9823"
FT		/db_xref="UNILIB:9699"
FT		/note="Vector: p773D-Pac (Pharmacia) with a modified
FT		polylinker; Site1: Not I; Site 2: EcoRI; The MI-P-NA is a
FT		normalized library comprised of anterior pituitary tissue
FT		at estrus days 0, 5, and 12. For a detailed description of
FT		the library from which this clone was derived, please
FT		visit our web site at http://pigast.genome.iasstate.edu/ .
FT		TAG_LIB=MI-P-NA TAG_TISSUE=anterior pituitary at estrus day
FT		12 TAG_SEQ=TCACAG"
FT		/organism="Sus scrofa"
FT		/strain="crossbred"
FT		/clone="MI-P-NA-aeg-e-07-1-UM.ab1"
FT		/clone_lib="MI-P-NA"
FT		/lab_host="DH10B (Life Technologies)"
XX		
XX	Sequence 308 BP: 134 A; 51 C; 57 G; 66 T; 0 other;	

XX	[1]
RN	1-659
RP	Kohara Y.;
RA	
RT	
RL	Submitted (10-JUL-2001) to the EMBL/GenBank/DDBJ databases.
RL	Yuji Kohara, National Institute of Genetics, Genome Biology Lab.; 1111
RL	Yata, Mishima, Shizuoka 411-8540, Japan (E-mail:ykohara@lab.nig.ac.jp,
XX	Tel.:81-559-81-6854, Fax:81-559-81-6855)
XX	
RN	[2]
RA	Kohara Y., Shin-i T., Thierry-Mieg J., Thierry-Mieg D., Suzuki Y.,
RA	Sugano S.;
RT	"A complementary view of the C.elegans genome.";
RL	Unpublished.
XX	
DR	UNILIB; 9635; 9635.
XX	
FH	Location/Qualifiers
FT	source
FT	1..659
FT	/db_xref="taxon:6239"
FT	/db_xref="UNILIB:9635"
FT	/sequenced_mol="cDNA to mRNA"
FT	/sex="Hermaphrodite"
FT	/organism="Caenorhabditis elegans"
FT	/clone="yk787h01"
FT	/clone_lib="unpublished oligo-capped cDNA library"
FT	/dev_stage="L4"
FT	/strain="N2"
FT	/tissue_type="whole animal"
XX	
SQ	Sequence 659 BP; 160 A; 162 C; 130 G; 205 T; 2 other;
	Query Match 1.7%; Score 35.2; DB 3; Length 659;
	Best Local Similarity 51.6%; Pred.No. 4;
	Matches 79; Conservative 0; Mismatched 74; Indels 0; Gaps 0;
Qy	1578 GTATCTGTGATAAAATCTCTTGAAAATACAGAAATCAAAAGGTTAATGATTTTTTGGTCAT 1637
Dd	165 GTTTCATTAAAAACAAATTGTAATTTCTTAATTTATCTTTATTCATTTTCTCTAT 106
Qy	1638 TCTGATTTGTCATTTTATTTATCTCGTTCATCGGTCAAAGTGAATTTACCCATTTGATTT 1697
Dd	105 CCCGATTATTCCTCTCCAGTTTGTGAACGCTTCAGTATCTCAGTCACAGAGTTTCATT 46
Qy	1698 TTCTGCTAGACAGATACTTTTAATTTTCAAA 1730
Dd	45 TATTGTTTCCACTTTAAATATTATTNAGTAA 13
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Bf	BF13200/c
ID	BF13200 standard; RNA; EST; 195 BP.
XX	
AC	BF13200;
XX	
SV	BF13200.1
XX	
DT	03-JAN-2001 (Rel. 66, Created)
DT	03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX	
DE	MI-P-O2-adg-f-01-I-UM.s1 MI-P-O2 Sus scrofa cDNA clone
DE	MI-P-O2-adg-f-01-I-UM 3', mRNA sequence.
XX	
KW	EST.
XX	
OS	Sus scrofa (pig)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC	Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX	
[1]	
RN	1-195


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RX MEDLINE; 97044477.
RA Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL discovery";
RL Genome Res. 6(9):791-806(1996).
DR UNILIB; 7284; 7284.
XX
CC Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. cDNA library Preparation: RJ Woods, JA Green, RS Prather S142
CC Animal Science Research Center, Department of Animal Science,
CC University of Missouri-Columbia, 65211 Clone distribution: clones
CC will be available through Research Genetics (www.resgen.com) The
CC following repetitive elements were found in this cDNA sequence:
CC 63-162, >(TAAAA)n#simple_repeat 85-158, >POLY_A#simple_repeat
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
XX Key Location/Qualifiers
FH
FH source
FH 1. .195
FH /db_xref="taxon:9823"
FH /db_xref="UNILIB:7284"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site 1: Not 1; Site 2: EcoRI; The MI-P-02
FH library is derived from ovary at estrus day 5. For a
FH detailed description of the library from which this clone
FH was derived, please visit our web site at
FH http://pigest.genome.iastate.edu/. TAG_SEQ=None found"
FH /organism="Sus scrofa"
FH /strain="crossbreed"
FH /clone="MI-P-02-ads-f-01-1-UM"
FH /clone_lib="MI-P-02"
FH /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 195 BP; 107 A; 14 C; 21 G; 53 T; 0 other;

Query Match 1.6%; Score 32.6; DB 9; Length 195;
Best Local Similarity 48.8%; Pred. No. 15;
Matches 89; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 1287 TTGGCTTTCTGTGCTGTTGATTTTGGCCAGATCGATCTGCATTATTGCTACTTTTCT 1346
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
194 TTGGCCCTGTGGTCCAGAACTCGAACCCCTGATTTTCTTTTCTTTTCTTTTCTTTT 135
QY 1347 ATGTATTATATCTCTGAGAGTCACATAAAGAGCATTTTTTTTGTGCAGCTATCA 1406
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
134 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 75
QY 1407 ATCGACTGATCTAATGTGAATAGTATCTCTTAAACAAAGCATCTATTTTGCGAG 1466
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
74 CGCATTTTATTCAATAAATAACTTCAGTAACAGCACTGTAAAGAGTGAACCTGTTAAA 15
QY 1467 AAA 1469
Db |||||
14 AAA 12

RESULT 4
BI400626/c
ID BI400626 standard; RNA; EST; 465 BP.
XX
AC BI400626;
XX

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SV BI400626.1
XX
DT 15-AUG-2001 (Rel. 68, Created)
DT 15-AUG-2001 (Rel. 68, Last updated, Version 1)
XX
DE MI-P-AV1-hqf-f-07-0-UI.s1 MI-P-AV1 Sus scrofa cDNA clone
DE MI-P-AV1-hqf-f-07-0-UI 3', mRNA sequence.
XX
KW EST.
XX
OS Sus scrofa (pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
RN [1]
RP 1-465
RX MEDLINE; 97044477.
RA Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL discovery";
RL Genome Res. 6(9):791-806(1996).
XX
DR UNILIB; 7287; 7287.
CC Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC normalized placenta library cDNA library Preparation: M.B. Soares
CC Lab, University of Iowa EST sequencing: M.B. Soares Lab, University
CC of Iowa Clone distribution: clones will be available through
CC Research Genetics (www.resgen.com) The following repetitive
CC elements were found in this cDNA sequence: 46-176.
CC >POLY_A#simple_repeat 405-452, >POLY_A#simple_repeat
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
XX Key Location/Qualifiers
FH
FH source
FH 1. .465
FH /db_xref="taxon:9823"
FH /db_xref="UNILIB:7287"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site 1: Not 1; Site 2: EcoRI; The MI-P-AV1
FH library is normalized library derived from the MI-P-AV0
FH library, ultimately derived from placenta tissue. For a
FH detailed description of the library from which this clone
FH was derived, please visit our web site at
FH http://pigest.genome.iastate.edu/. The procedure used to
FH create this library has been previously described (Bonaldo
FH , Lennon and Soares, Genome Research 6: 791-806, 1996)
FH TAG_LIB=MI-P-AV1 TAG_TISSUE=placenta TAG_SEQ=ATTGG"
FH /organism="Sus scrofa"
FH /strain="crossbreed"
FH /clone="MI-P-AV1-hqf-f-07-0-UI"
FH /clone_lib="MI-P-AV1"
FH /lab_host="DH10B (Life Technologies)"
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SQ Sequence 465 BP; 255 A; 83 C; 74 G; 53 T; 0 other;

Query Match 1.6%; Score 32.2; DB 9; Length 465;
Best Local Similarity 54.7%; Pred. No. 15;
Matches 64; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1641 GATTTGTCATTTTATTATCTGTTATCGTCTAAAGTCTAATTTACCCATTTTTC 1700

```



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RP 1-136
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferstutz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC r1 sequence also available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1. .136
FH /db_xref="taxon:9606"
FH /organism="Homo sapiens"
FH /clone_lib="434 (synonym: htes3). Vector pSport1; host
FH DH10B; sites NotI + SalI"
FH /dev_stage="adult"
FH /tissue_type="testis"
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SQ Sequence 136 BP; 8 A; 4 C; 4 G; 119 T; 1 other;

Query Match 1.5%; Score 31.2; DB 2; Length 136;
Best Local Similarity 53.2%; Pred. No. 28;
Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 1639 CTGATTGTCATTTTATCTGTTATCGGTCCTAAAGTCTAAATTTACCCATTTGATTTT 1698
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8 CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 67

Qy 1699 TCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGCAGACACTTTTTTTTTTTT 1758
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 127

Qy 1759 AAAA 1762
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Db 128 AAAA 131

RESULT 9
BF712847/c standard; RNA; EST; 374 BP.
XX
AC BF712847;
XX
SV BF712847.1
XX
03-JAN-2001 (Rel. 66, Created)
DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX
MI-P-Ol-ado-e-09-1-UM.s1 MI-P-Ol Sus scrofa cDNA clone
DE MI-P-Ol-ado-e-09-1-UM.3', mRNA sequence.
XX
KW EST.
XX
Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
[1]
RP 1-374
RX MEDLINE; 97044477.
RA Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RT discovery";
RL Genome Res. 6(9):791-806(1996).
XX
XX UNILIB; 7283; 7283.

```

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CC Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142
CC Animal Science Research Center, Department of Animal Science,
CC University of Missouri-Columbia, 65211 Clone distribution: clones
CC will be available through Research Genetics (www.resgen.com) The
CC following repetitive elements were found in this cDNA sequence:
CC 39-154, >POLY_A#Simple repeat 254-359, >POLY_A#Simple_repeat
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
FH Key Location/Qualifiers
FH source 1. .374
FH /db_xref="taxon:9823"
FH /db_xref="UNILIB:7283"
FH /note="Vector: p773D-pac (Pharmacia) with a modified
FH polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-Ol
FH library is derived from ovary at estrus day 0. For a
FH detailed description of the library from which this clone
FH was derived, please visit our web site at
FH http://pigest.genome.iastate.edu/. TAG_SEQ=None found"
FH /organism="Sus scrofa"
FH /strain="crossbreed"
FH /clone="MI-P-Ol-ado-e-09-1-UM"
FH /clone_lib="MI-P-Ol"
FH /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 374 BP; 224 A; 29 C; 72 G; 49 T; 0 other;

Query Match 1.5%; Score 31.2; DB 9; Length 374;
Best Local Similarity 52.3%; Pred. No. 24;
Matches 69; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 1626 TTTTGTTCATTCGTGATTTGTCATTTTATATCTGTTATCGGTCCTAAAGTGTCTAATTTA 1685
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223 TTTTGTTCATTCGTGATTTGTCATTTTATATCTGTTATCGGTCCTAAAGTGTCTAATTTA 164
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 1686 CCCATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGCAGACACTTTT 1745
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 163 TTTTTCCAATTTTTCCTCCCTTTTGTGTTTAAATTCCTGTTTTCCTCTTTT 104
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 1746 TTTTGTTCATTTT 1757
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 103 TTTTGTTCATTTT 92

RESULT 10
HSM002682/c
ID HSM002682 standard; RNA; EST; 472 BP.
XX
AC AL038339;
XX
SV AL038339.1
XX
12-MAR-1999 (Rel. 59, Created)
DT 25-SEP-1999 (Rel. 61, Last updated, Version 3)
XX
Homo sapiens mRNA; EST DKFZp566K192_r1 (from clone DKFZp566K192)
XX EST; expressed sequence tag.
XX
Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```
XX RN 1-472
RA OTtenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RT Submitted (24-SEP-1999) to the EMBL/GenBank/DBS databases.
RL MIPS, Am Klopferspitz 18a, D-82152 Martinsried, GERMANY
XX DR RZPD; DKFZp566K192; DKFZp566K192.
XX This is the 5' sequence of the clone insert
CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC sequenced by MedGenomix within the cDNA sequencing consortium
CC of the German Genome Project.
CC s1 sequence also available.
CC This clone is available at the RZPD in Berlin.
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key Location/Qualifiers
FT source 1. 472
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp566K192"
FT /clone_lib="566 (synonym: h6kd2). Vector pAMP1; host
FT Xl-2blue; sites NotI + SalI"
FT /dev_stages="fetal"
FT /tissue_type="kidney"
XX Sequence 472 BP; 99 A; 154 C; 100 G; 119 T; 0 other;

Query Match 1.5%; Score 31; DB 2; Length 472;
Best Local Similarity 53.8%; Pred. No. 25;
Matches 64; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 721 TCCATCTGCTGTAGCACAGACGCGCTGGACAGCGCCCTTCGGCTGCATG 780
DB 234 TCCATGGTGGCTAGGTGAGTGTGAGGGGTGAGTGGCTGCTCAGCTCCCTCAGCTGCAGC 175
QY 781 AGCAGCAAGGGGCGCCCTTACCTGCTCTTCAGCGTCAATGGGAGTGGGCAATTTTGTGG 839
DB 174 TACAGCAGCGCCCTTATATATATGCAAGCTTCTGGAAGCTTCTGGAATGGTATGTCAGGGG 116

RESULT 11
BF712218/c
ID BF712218 standard; RNA; EST; 400 BP.
XX AC BF712218;
XX SV BF712218.1
XX 03-JAN-2001 (Rel. 66, Created)
DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX MI-P-A3-add-a-08-1-UM.s1 MI-P-A3 Sus scrofa cDNA clone
DE MI-P-A3-add-a-08-1-UM 3', mRNA sequence.
XX EST.
XX Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
RN 1-400
RP MEDLINE; 97044477.
RX Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RT discovery";
```

```
RL Genome Res. 6(9):791-806(1996).
XX UNILIB; 7273; 7273.
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Klidde Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized anterior pituitary at estrus day 12 library cDNA
CC Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal
CC Science Research Center, Department of Animal Science, University
CC of Missouri-Columbia, 65211 Clone distribution: clones will be
CC available through Research Genetics (www.resgen.com) The following
CC repetitive elements were found in this cDNA sequence: 1-25,
CC >AT_rich#Low_complexity 32-90, >AT_rich#Low_complexity 102-136,
CC >AT_rich#Low_complexity
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX Key Location/Qualifiers
FT source 1. 400
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7273"
FT /note="vector: p7T73D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-A3
FT library is derived from anterior pituitary at estrus day
FT 12. For a detailed description of the library from which
FT this clone was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. TAG LIB=MI-P-A3
FT TAG TISSUE=anterior pituitary at estrus day 12
FT TAG_SEQ=TGACAG"
FT /organism="Sus scrofa"
FT /strain="crossbreed"
FT /clone="MI-P-A3-add-a-08-1-UM"
FT /clone_lib="MI-P-A3"
FT /lab_host="DH10B (Life Technologies)"
XX Sequence 400 BP; 175 A; 39 C; 75 G; 111 T; 0 other;

Query Match 1.5%; Score 30.8; DB 9; Length 400;
Best Local Similarity 55.7%; Pred. No. 27;
Matches 59; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1551 AAACCATGAGTCATTTGTCATTAGAGTATTCGTATAAAATCTCTTGAAATACCTGAAA 1610
DB 181 AAACCCCGCTTGATTTGGGTTTTCACCAAAATTTTAAATGCGCTTTTAAATTAATAAAA 122
QY 1611 TCAAAAGGTTAATGATTTTGTTCATTCTGATTTGTCATTTATT 1656
DB 121 ACCTTTTAAAAAAATTTTGGGCGCTTCCTTTTATTATTTT 76

RESULT 12
BF703505/c
ID BF703505 standard; RNA; EST; 502 BP.
XX AC BF703505;
XX SV BF703505.1
XX 26-DEC-2000 (Rel. 66, Created)
DT 26-DEC-2000 (Rel. 66, Last updated, Version 1)
XX MI-P-H1-abm-b-03-1-UM.s1 MI-P-H1 Sus scrofa cDNA clone
DE
```


QY	1739	ACACTTTTATTTTTTTTTT	1757
Db	131	AAAAATTTTTTTTTTTTTT	113
RESULT 14			
Bf713152/c			
ID	Bf713152	standard; RNA; EST; 512 BP.	
XX	AC		
XX	Bf713152;		
SX			
VV	Bf713152.1		
XX			
DT	03-JAN-2001	(Rel. 66, Created)	
DT	03-JAN-2001	(Rel. 66, Last updated, Version 1)	
XX			
DE	MI-P-Ol-adq-a-01-l-UM s1 MI-P-Ol Sus scrofa cDNA clone		
DE	MI-P-Ol-adq-a-01-l-UM 3', mRNA sequence.		
XX			
KW	EST.		
XX			
Sus scrofa (pig)			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;		
OC	Eucheria; Cetartiodactyla; Suina; Suidae; Sus.		
XX	[1]		
RN	1-512		
RP	MEDLINE; 97044477.		
RX	Bonaldo M.F., Lennon G., Soares M.B.;		
RA	"Normalization and subtraction: two approaches to facilitate gene		
RT	discovery";		
RL	Genome Res. 6(9):791-806(1996).		
XX			
DR	UNILIB; 7283; 7283.		
CC	Contact: Tuggle CK		
CC	Molecular Genetics Laboratory, Department of Animal Science		
CC	Iowa State University		
CC	201 Kildes Hall, Ames, IA 50011-3150, USA		
CC	Tel: 5152944252		
CC	Fax: 5152942401		
CC	Email: cktuggl@iastate.edu		
CC	The sequence contained an oligo-dT track that was present in the		
CC	oligonucleotide that was used to prime the synthesis of first		
CC	strand cDNA and therefore this may represent a bonafide poly A		
CC	tail. The sequence tag present in the cDNA between the NotI site		
CC	and the oligo-dt track served to verify it as a clone from the		
CC	non-normalized ovary at estrus day 0 library cDNA library		
CC	Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science		
CC	Research Center, Department of Animal Science, University of		
CC	Missouri-Columbia, 65211 Clone distribution: clones will be		
CC	available through Research Genetics (www.resgen.com)		
CC	Seq primer: M13 Forward		
CC	POLYA=yes.		
XX			
FF	Key	Location/Qualifiers	
FT	source		
FT	1..512		
FT	/db_xref=taxon:9823"		
FT	/db_xref=UNILIB:7283"		
FT	/note=vector: pT7T3D-Pac (Pharmacia) with a modified		
FT	polylinker; Site 1: Not I; Site 2: EcoRI; The MI-p-Ol		
FT	library is derived from ovary at estrus day 0. For a		
FT	detailed description of the library from which this clone		
FT	was derived, please visit our web site at		
FT	http://pigest.genome.iastate.edu/. TAG LIB=MI-P-Ol		
FT	TAG TISSUE=ovary at estrus day 0 TAG_SEQ=GACGTA"		
FT	/organism="Sus scrofa"		
FT	/strain="crossbreed"		
FT	/clones="MI-P-Ol-adq-a-01-l-UM"		
FT	/clone_lib="MI-P-Ol"		
FT	/lab_host="DH10B (Life Technologies)"		
XX			


```
Query Match      1.5%; Score 29.6; DB 2; Length 127;
Best Local Similarity 52.5%; Pred. No. 56;
Matches 62; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1643 TTGTGCTATTTTATCTGTTATCGTCTAAAGTGTAAATTTACCCATTTGATTTTCTG 1702
DB 10 TTTTNTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 69

QY 1703 CTAGACAGATAACTTTTAATTTTCAAAATTTGGCAGACACTTTTTTTTTTTTTTTGAA 1760
DB 70 TTTTNTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 127

RESULT 18
HSM003359/c
ID HSM003359 standard; RNA; EST; 147 BP.
XX
AC AL038883;
XX
SV AL038883.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp566E0247_r1 (from clone DKFZp566E0247)
XX
KW EST; expressed sequence tag.
XX
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX [1]
RN 1-147
RA Ottenwaelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by MediGenomix within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
FH source 1..147
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp566E0247"
FT /clone_lib="566 (synonym: hfkd2). Vector pAMP1; host
FT XI-2blue; sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="kidney"
XX
SQ Sequence 147 BP; 94 A; 14 C; 12 G; 27 T; 0 other;

Query Match      1.4%; Score 29.4; DB 2; Length 147;
Best Local Similarity 54.1%; Pred. No. 59;
Matches 60; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1293 TTTCTGTCCTGATTTTTCGCCAGATGATTCGATTTATTTGTTACTTTTCTATCTAT 1352
DB 145 TTTTNTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 86

QY 1353 TATAATCCTGTAGAGTCACATAAAGGAGTATTTTTTTTTCGACCTTA 1403
DB 85 TTTTNTTAAAGAGAGGTCCAAATCAATAGTCTTTTATTGCATCATTTAA 35

RESULT 19
1.4%; Score 29.4; DB 9; Length 150;
Query Match
SQ Sequence 150 BP; 71 A; 4 C; 20 G; 55 T; 0 other;
```

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BF711427/c
ID BF711427 standard; RNA; EST; 150 BP.
XX
AC BF711427;
XX
SV BF711427.1
XX
XX 03-JAN-2001 (Rel. 66, Created)
DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX
DE MI-P-A2-acp-e-06-1-UM.sl MI-P-A2 Sus scrofa cDNA clone
DE MI-P-A2-acp-e-06-1-UM 3', mRNA sequence.
XX
XX EST.
XX
XX Sus scrofa (pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
XX [1]
RN 1-150
RA Ronaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL Genome Res. 6(9):791-806(1996).
XX
XX UNILIB; 7272; 7272.
XX
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized anterior pituitary at estrus day 5 library cDNA
CC Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal
CC Science Research Center, Department of Animal Science, University
CC of Missouri-Columbia, 65211 Clone distribution: clones will be
CC available through Research Genetics (www.resgen.com) The following
CC repetitive elements were found in this cDNA sequence: 27-80,
CC >POLY_A#Simple_repeat
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
XX Key Location/Qualifiers
FH source 1..150
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7272"
FT /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-A2
FT library is derived from anterior pituitary at estrus day 5.
FT For a detailed description of the library from which this
FT clone was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. TAG LIB=MI-P-A2
FT TAG TISSUE=anterior pituitary at estrus day 5
FT TAG_SEQ=TCGCGT"
FT /organism="Sus scrofa"
FT /strain="crossbred"
FT /clone="MI-P-A2-acp-e-06-1-UM"
FT /clone_lib="MI-P-A2"
FT /lab_host="DH10B (Life Technologies)"
XX
XX Sequence 150 BP; 71 A; 4 C; 20 G; 55 T; 0 other;
SQ
Query Match
1.4%; Score 29.4; DB 9; Length 150;
```

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Best Local Similarity 66.7%; Pred. No. 59;
Matches 42; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1705 AGACAGATAACTTTTAAATTTTCAAAATTTGGCAGACACTTTTTTTTTTTTTTTTTCGAAATC 1764
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 90 AGTGAATAATTTCCCTTTTGTGTTTGTTCCTTTTCCATTTTATTTTATTTTAAAT 31

QY 1765 TTT 1767
    |||
Db 30 TTT 28

RESULT 20
BF712867/c standard; RNA; EST; 414 BP.
XX AC BF712867;
XX AC BF712867;
SV BF712867.1
XX 03-JAN-2001 (Rel. 66, Created)
DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX MI-P-Ol-ado-h-08-1-UM.s1 MI-P-Ol Sus scrofa cDNA clone
DE MI-P-Ol-ado-h-08-1-UM 3', mRNA sequence.
XX KW EST.
XX Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
RN 1-414
RP MEDLINE; 97044477.
RX Bonaldo M.F., Lennon G., Soares M.B.;
RA "Normalization and subtraction: two approaches to facilitate gene
RT discovery";
RL Genome Res. 6(9):791-806(1996).
XX UNILIB; 7283; 7283.
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. cDNA library Preparation: RJ Woods, JA Green, RS Prather S142
CC Animal Science Research Center, Department of Animal Science,
CC University of Missouri-Columbia, 65211 Clone distribution: clones
CC will be available through Research Genetics (www.resgen.com) The
CC following repetitive elements were found in this cDNA sequence:
CC 209-313 >POLY.A#Simple_repeat 366-405, >AT_rich#Low_complexity
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX Key Location/Qualifiers
FH source 1. .414
FT /db_xref="taxon:9823"
FT /notes="vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not 1; Site 2: EcoRI; The MI-P-Ol
FT library is derived from ovary at estrus day 0. For a
FT detailed description of the library from which this clone
FT was derived, please visit our web site at
FT http://pigsc.genome.iastate.edu/. TAG_SEQ=None found"
FT /organism="Sus scrofa"
```

```
FT /strain="crossbreed"
FT /clone="MI-P-Ol-ado-h-08-1-UM"
FT /clone_lib="MI-P-Ol"
FT /lab_host="DH10B (Life Technologies)"
XX Sequence 414 BP; 189 A; 46 C; 83 G; 96 T; 0 other;

Query Match 1.4%; Score 29.4; DB 9; Length 414;
Best Local Similarity 47.1%; Pred. No. 49;
Matches 90; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1564 TTTTGTCATTTAGAGTATTCGTATAAATCTTTGAAAATCTGAAAATCAAAAGGTTAAT 1623
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 399 TTTTATTTTACCAAAATTTTGAATTTTTTTTTTCCCTTCCAAAAAATAAATTTTCG 340
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1624 GATTTTTTGTTCATTCGTGATTTCGCTATTTATTTATCTGTTATCGTCTAAAGTCCTAAT 1683
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 339 GGTTTTTCCCGGTTTCCCTTAAATAATTTTTTTCCTTTTTTTTTTAAAGTTTTTCCT 280
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1684 TACCATTTGATTTTTCTGCTAGACAGATAACTTTTAAATTTTCAAAATTTGGCAGACACT 1743
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 279 TCCCTTTTGGGGTATTTTTTCCGTTTCAAAATCCCTTTACCCAATACCTTTTTTTT 220
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1744 TTTTTTTTTTTT 1754
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 219 TTGTTTTTTTTT 209

RESULT 21
BF704037/c standard; RNA; EST; 417 BP.
XX AC BF704037;
XX AC BF704037.1
SV BF704037.1
XX 26-DEC-2000 (Rel. 66, Created)
DT 26-DEC-2000 (Rel. 66, Last updated, Version 1)
XX MI-P-A3-abw-c-09-1-UM.s1 MI-P-A3 Sus scrofa cDNA clone
DE MI-P-A3-abw-c-09-1-UM 3', mRNA sequence.
XX KW EST.
XX Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
RN 1-417
RP MEDLINE; 97044477.
RX Bonaldo M.F., Lennon G., Soares M.B.;
RA "Normalization and subtraction: two approaches to facilitate gene
RT discovery";
RL Genome Res. 6(9):791-806(1996).
XX UNILIB; 7273; 7273.
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized anterior pituitary at estrus day 12 library cDNA
CC Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal
CC Science Research Center, Department of Animal Science, University
```

CC of Missouri-Columbia, 65211 Clone distribution: clones will be
 CC available through Research Genetics (www.resgen.com) The following
 CC repetitive elements were found in this cDNA sequence: 1-29,
 CC >AT rich#Low complexity 56-193, >POLY_A#Simple_repeat
 CC Seq primer: M13 Forward
 CC POLYA=Yes.

XX FH Key Location/Qualifiers
 FT source
 FT 1. .417
 FT /db_xref="taxon:9823"
 FT /db_xref="UNILIB:7273"
 FT /note=Vector: pT73D-Pac (Pharmacia) with a modified
 FT polylinker; Site 1: Not 1; Site 2: EcoRI; The MI-P-A3
 FT library is derived from anterior pituitary at estrus day
 FT 12. For a detailed description of the library from which
 FT this clone was derived, please visit our web site at
 FT http://pigest.genome.iastate.edu/. TAG_LIB=MI-P-A3
 FT TAG_TISSUE=anterior pituitary at estrus day 12
 FT TAG_SEQ=TGACAG
 FT /organism="Sus scrofa"
 FT /strain="crossbreed"
 FT /clone="MI-P-A3-abw-c-09-1-UM"
 FT /clone_lib="MI-P-A3"
 FT /lab_host="DH10B (Life Technologies)"

XX SQ Sequence 417 BP; 219 A; 65 C; 70 G; 61 T; 2 other;
 Query Match 1.4%; Score 29.4; DB 9; Length 417;
 Best Local Similarity 66.7%; Pred. No. 49; Mismatches 21; Indels 0; Gaps 0;
 Matches 42; Conservative 0;

QY 1695 TTTTCTGCTAGACAGATACTTTAAATTTTCAAAATTTGGCAGACACTTTTTTTTTTT 1754
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 242 TTTTGGCTTTGGAAAAAATTTTTCCTTCCCTTCCAGAAAAATTTTTTTTTT 183

QY 1755 TTT 1757
 |||||
 Db 182 TTT 180

RESULT 22
 HSM001232/c
 ID HSM001232 standard; RNA; EST; 144 BP.
 XX AC AL036913;
 XX SV AL036913.1
 XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX Homo sapiens mRNA; EST DKFZp564B1164_x1 (from clone DKFZp564B1164)
 XX EST; expressed sequence tag.

XX KW Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX [1]
 RN 1-144
 RP Dueterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
 RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY
 XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No sl sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX FH Key Location/Qualifiers
 FT source
 FT 1. .144
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp564B1164"
 FT /clone_lib="564 (synonym: hEhr2). Vector pAMP1; host
 FT X1-2blue; sites NotI + Sali"
 FT /dev stages="fetal"
 FT /tissue_type="brain"

XX SQ Sequence 144 BP; 119 A; 8 C; 4 G; 5 T; 8 other;
 Query Match 1.4%; Score 29.2; DB 2; Length 144;
 Best Local Similarity 49.6%; Pred. No. 64;
 Matches 64; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1605 CTGAATCAAAAGGTAATGATTTTGTTCATTCGATTTGTCATTTATTATCTGTTA 1664
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 137 CNGNTNNNNAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 78

QY 1665 TCGGCTAAAGTCTAAATTTACCCATTTGATTTTCTGCTAGACAGATACTTTTAATTT 1724
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 77 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 19

QY 1725 TTCAAAATTT 1733
 |||||
 Db 17 TTTTTTTTT 9

RESULT 23
 BF713586/c
 ID BF713586 standard; RNA; EST; 206 BP.
 XX AC BF713586;
 XX SV BF713586.1
 XX 03-JAN-2001 (Rel. 66, Created)
 DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
 XX MI-P-O2-adx-d-09-1-UM.sl MI-P-O2 Sus scrofa cDNA clone
 DE MI-P-O2-adx-d-09-1-UM 3', mRNA sequence.
 XX EST.

XX OS Sus scrofa (pig)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 XX [1]
 RN 1-206
 RP MEDLINE; 97044477.
 RA Ronaldo M.F., Lennon G., Soares M.B.;
 RT "Normalization and subtraction: two approaches to facilitate gene
 RT discovery";
 RL Genome Res. 6(9):791-806(1996).
 XX UNILIB; 7284; 7284.
 XX Contact: Tuggle CK
 CC Molecular Genetics Laboratory, Department of Animal Science
 CC Iowa State University
 CC 201 Kildee Hall, Ames, IA 50011-3150, USA
 CC Tel: 5152944252
 CC Fax: 5152942401
 CC Email: cktuggle@iastate.edu
 CC The sequence contained an oligo-dT track that was present in the
 CC oligonucleotide that was used to prime the synthesis of first
 CC strand cDNA and therefore this may represent a bonafide poly A
 CC tail. cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142
 CC Animal Science Research Center, Department of Animal Science,

OS Sus scrofa (pig)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eukarya; Cetartiodactyla; Suina; Suidae; Sus.
 XX [1]
 RN 1-385
 RP MEDLINE; 97044477.
 RX Bonaldo M.F., Lennon G., Soares M.B.;
 RA "Normalization and subtraction: two approaches to facilitate gene
 RT discovery";
 RL Genome Res. 6(9):791-806(1996).
 XX UNILIB; 7284; 7284.
 DR
 XX
 CC Contact: Tuggle CK
 CC Molecular Genetics Laboratory, Department of Animal Science
 CC Iowa State University
 CC 201 Kildee Hall, Ames, IA 50011-3150, USA
 CC Tel: 5152944252
 CC Fax: 5152942401
 CC Email: cktuggle@iastate.edu
 CC The sequence contained an oligo-dT track that was present in the
 CC oligonucleotide that was used to prime the synthesis of first
 CC strand cDNA and therefore this may represent a bonafide poly A
 CC tail. The sequence tag present in the cDNA between the NotI site
 CC and the oligo-dT track served to verify it as a clone from the
 CC non-normalized ovary at estrus day 5 library cDNA library
 CC Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science
 CC Research Center, Department of Animal Science, University of
 CC Missouri-Columbia, 65211 Clone distribution: clones will be
 CC available through Research Genetics (www.resgen.com) The following
 CC repetitive elements were found in this cDNA sequence: 1-34,
 CC >AT rich#Low complexity
 CC Seq primer: M13 Forward
 CC POLYA=yes.
 XX
 FH Key Location/Qualifiers
 FT source 1..385
 FT /db_xref="taxon:9823"
 FT /db_xref="UNILIB:7284"
 FT /note="Vector: pT73D-Pac (Pharmacia) with a modified
 FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-02
 FT library is derived from ovary at estrus day 5. For a
 FT detailed description of the library from which this clone
 FT was derived, please visit our web site at
 FT http://pigest.genome.iastate.edu/. TAG_LIB=MI-P-02
 FT TAG_ISSUE=ovary at estrus day 5 TAG_SEQ=ATCATC"
 FT /organism="Sus scrofa"
 FT /strains="crossbreed"
 FT /clone="MI-P-02-abr-e-09-1-UM"
 FT /clone_lib="MI-P-02"
 FT /lab_host="DH10B (LIFE Technologies)"
 XX
 SQ Sequence 385 BP; 116 A; 66 C; 80 G; 123 T; 0 other;
 Query Match 1.4%; Score 29.2; DB 9; Length 385;
 Best Local Similarity 51.5%; Pred. No. 54;
 Matches 67; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
 QY 1293 TTTCTGTGTTGATTTTGGCCAGATGATCTGCAATTTATTTGTACTTTTCTATGTAT 1352
 DB |||||
 2 TTTTCTTTTATTTATGATTTTATTAATTTGCTTTTACAGATTTTACAAGGCAATGAT 61
 QY 1353 TATAATCTGTAGAAGTCACTAATAAGGAGTATTTTTTTTGTGACGTTATCAATCAGA 1412
 DB |||||
 62 TATTTATCACTCCAGTCGGTATCAAGAAATAACTCTTTTCCAGTATATTTGATTTT 121
 QY 1413 CTGATCTAAT 1422
 DB |||||
 122 TTTATGATTT 131

RESULT 26
 BM377646/c
 ID BM377646 standard; RNA; EST; 422 BP.
 XX
 AC BM377646;
 XX
 SV BM377646.1
 XX
 15-JAN-2002 (Rel. 70, Created)
 DT 15-JAN-2002 (Rel. 70, Last updated, Version 1)
 XX
 DE EBem04 SQ003 M04 R IGF Barley EBem04 library Hordeum vulgare cDNA clone
 DE EBem04_SQ003_M04_5', mRNA sequence.
 XX
 KW EST.
 XX
 OS Hordeum vulgare
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
 OC Triticeae; Hordeum.
 XX
 RN [1]
 RP 1-422
 RA Hedley P., Liu H., Caldwell D., McCallum N., Mudie S., Cardie L.,
 RA Ramsay L., Machray G., Marshall D.F.M., Waugh R.;
 RT "Development of Barley Transcriptome Resources";
 RL Unpublished.
 XX
 DR UNILIB; 9790; 9790.
 XX
 CC Contact: Waugh R
 CC Unit of Genomics
 CC Scottish Crop Research Institute
 CC Invergowrie, Dundee, DD2 5DA, Scotland, UK
 CC Tel: 00 44 1382 562731
 CC Fax: 00 44 1382 562426
 CC Email: rwaugh@scri.sari.ac.uk
 CC All sequence has a Phred quality score of 20 or over
 CC Seq primer: M13 reverse.
 XX
 FH Key Location/Qualifiers
 FT source 1..422
 FT /db_xref="taxon:4513"
 FT /db_xref="UNILIB:9790"
 FT /note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
 FT Non-normalised library, directionally cloned into pSPORT1.
 FT Derived from embryos dissected from developing grains (12
 FT days post anthesis) in glasshouse grown barley plants.
 FT Developed as part of the barley transcriptome resources of
 FT BBSRC/SEERAD funded cereal IGP (Investigating Gene
 FT Function) project."
 FT /organism="Hordeum vulgare"
 FT /cultivar="Optic"
 FT /clone="EBem04 SQ003 M04"
 FT /clone_lib="IGF Barley EBem04 library"
 FT /tissue_type="Embryo"
 FT /dev_stage="12 days post anthesis"
 FT /lab_host="DH10B"
 XX
 SQ Sequence 422 BP; 99 A; 166 C; 87 G; 70 T; 0 other;
 Query Match 1.4%; Score 29.2; DB 6; Length 422;
 Best Local Similarity 59.8%; Pred. No. 53;
 Matches 49; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 1830 GCTGGATGCTGTGGGGCATGATGTGTGGAGGAAGTGAAGTCTTTAGGTCGTCTCA 1889
 DB |||||
 161 GCAGGATGCGTTGACGGAGAGTACAGGACGTTCTTGATGAGCTGCAGGCTTTCT 102
 QY 1890 GGGTCGGGCAATCTTTTGTGTT 1911
 DB |||||
 101 TGGTGGGCGGTTTGTCTGTT 80

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RESULT 27
BF711499/c standard; RNA; EST; 445 BP.
XX BF711499
AC BF711499;
SV BF711499.1
XX
DT 03-JAN-2001 (Rel. 66, Created)
DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX
DE MI-P-A2-acq-a-12-1-UM.s1 MI-P-A2 Sus scrofa cDNA clone
DE MI-P-A2-acq-a-12-1-UM 3', mRNA sequence.
XX
XX
XX EST.
XX
XX Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
XX [1]
RN 1-445
RX MEDLINE; 97044477.
RA Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RT discovery";
RL Genome Res. 6(9):791-806(1996).
XX
XX UNILIB; 7272; 7272.
XX
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: ktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized anterior pituitary at estrus day 5 library cDNA
CC Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal
CC Science Research Center, Department of Animal Science, University
CC of Missouri-Columbia, 65211 Clone distribution: clones will be
CC available through Research Genetics (www.resgen.com) The following
CC repetitive elements were found in this cDNA sequence: 19-154,
CC >POLY_A#Simple_repeat 234-288, >POLY_A#Simple_repeat 295-319,
CC >GC_richLow_complexity
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
XX Key Location/Qualifiers
FH source 1..445
FH /db_xref="taxon:9823"
FH /db_xref="UNILIB:7272"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-A2
FH library is derived from anterior pituitary at estrus day 5.
FH For a detailed description of the library from which this
FH clone was derived, please visit our web site at
FH http://pigest.genome.iastate.edu/. TAG LIB=MI-P-A2
FH TAG TISSUE=anterior pituitary at estrus day 5
FH TAG_SEQ=TCGCGT"
FH /organism="Sus scrofa"
FH /strain="crossbreed"
FH /clone="MI-P-A2-acq-a-12-1-UM"
FH /clone_lib="MI-P-A2"
FH /lab_host="DH10B (Life Technologies)"

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XX
SQ Sequence 445 BP; 218 A; 84 C; 106 G; 37 T; 0 other;
Query Match 1.4%; Score 29.2; DB 9; Length 445;
Best Local Similarity 53.5%; Pred. No. 53;
Matches 61; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 1617 GGTAAATGATTTTGTTCATTCGATTTTCATTTTATTCATCGTCTAAAGT 1676
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 127 GGTITTTTTTTTTTGGCGCTGGGGTTTTTTTTTTTTTTGGGGCCCCCTTTTTT 68
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1677 GCTAAATTTACCATTTGATTTTCTGCTAGACAGATAACTTTTAATTTTCAAA 1730
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 67 TCTTTTTTCCCGCGTTTTTTTTTTTCTAAGGGGTTTTTTTTTTTTTTTAAAAA 14
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
RESULT 28
BF702714/c standard; RNA; EST; 311 BP.
XX ID BF702714
XX AC BF702714;
XX SV BF702714.1
XX
DT 25-DEC-2000 (Rel. 66, Created)
DT 25-DEC-2000 (Rel. 66, Last updated, Version 1)
XX
DE MI-P-E3-aam-f-04-1-UM.s1 MI-P-E3 Sus scrofa cDNA clone
DE MI-P-E3-aam-f-04-1-UM 3', mRNA sequence.
XX
XX EST.
XX
XX Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
XX [1]
RN 1-311
RX MEDLINE; 97044477.
RA Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RT discovery";
RL Genome Res. 6(9):791-806(1996).
XX
XX UNILIB; 7275; 7275.
XX
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: ktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142
CC Animal Science Research Center, Department of Animal Science,
CC University of Missouri-Columbia, 65211 Clone distribution: clones
CC will be available through Research Genetics (www.resgen.com) The
CC following repetitive elements were found in this cDNA sequence:
CC 17-138, >POLY_A#Simple_repeat 266-294, >GC_richLow_complexity
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
XX Key Location/Qualifiers
FH source 1..311
FH /db_xref="taxon:9823"
FH /db_xref="UNILIB:7275"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-E3
FH library is derived from fetus at gestational day 45. For a

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CC	Iowa State University
CC	201 Kildee Hall, Ames, IA 50011-3150, USA
CC	Tel: 5152944252
CC	Fax: 5152942401
CC	Email: cktuggle@iastate.edu
CC	The sequence contained an oligo-dT track that was present in the
CC	oligonucleotide that was used to prime the synthesis of first
CC	strand cDNA and therefore this may represent a bonafide poly A
CC	tail. cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142
CC	Animal Science Research Center, Department of Animal Science,
CC	University of Missouri-Columbia, 65211 Clone distribution: clones
CC	will be available through Research Genetics (www.resgen.com) The
CC	following repetitive elements were found in this cDNA sequence:
CC	1-22, >AT_rich#Low_complexity 46-131, >POLY_A#Simple_repeat 293-409
CC	>POLY_A#Simple_repeat
CC	Seq primer: M13 Forward
CC	POLYA=Yes.
XX	
XX	Key Location/Qualifiers
PH	source
FT	1..428
FT	/db_xref=taxon:9823"
FT	/db_xref=UNILIB:7285"
FT	/note=Vector: pT73D-Pac (Pharmacia) with a modified
FT	polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-O3
FT	library is derived from ovary at estrus day 12. For a
FT	detailed description of the library from which this clone
FT	was derived, please visit our web site at
FT	http://pigest.genome.iastate.edu/. TAG_SEQ=None found"
FT	/organism=Sus scrofa"
FT	/strain=Crossbred"
FT	/clone=MI-P-O3-aba-g-03-1-UM"
FT	/clone_lib=MI-P-O3"
FT	/lab_host=DH10B (Life Technologies)"
XX	
SQ	Sequence 428 BP; 217 A; 98 C; 62 G; 51 T; 0 other;
	Query Match 1.4%; Score 29; DB 9; Length 428;
	Best Local Similarity 49.0%; Pred.No. 58;
	Matches 77; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY	1617 GGTTAATGATTTTTTGTCATTCTGAATTTGTCTATTTTATTATCTGTTATCGGTCTAAAGT 1676
Db	197 GGTTTTTTTTTTTTTCCCCCCCCTTTTTTGGGGTGTTTTTTTTTAAAAAGGGGGG 138
QY	1677 GCTAATTTACCAATTTGATTTTCTCTAGACAGATAACTTTTAATTTTCAAATTTGCC 1736
Db	137 GGGGGGTGTTTTTTTTTTTTTTTTTTTTTTAAAAAAAAGAATTTTTTTTTTTTGTTC 78
QY	1737 AGACACATTTTTTTTTTTTTTTTGAATAATCTTCTCCTCC 1773
Db	77 CCCGTTTTTTTCCCTTTTTTTTTTTTTTTTATTTTCCCCC 41
RESULT 31	
BI400750/c	
ID BI400750	standard; RNA; EST; 576 BP.
XX AC	BI400750;
XX SV	BI400750.1
XX DT	15-AUG-2001 (Rel. 68, Created)
XX DE	15-AUG-2001 (Rel. 68, Last updated, Version 1)
DE DE	MI-P-AV1-nqh-b-12-0-UI.s1 MI-P-AV1 Sus scrofa cDNA clone
DE DE	MI-P-AV1-nqh-b-12-0-UI 3', mRNA sequence.
XW	EST.
XX OS	Sus scrofa (pig)
XX OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC OC	Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

XX	[1]
RN	1-576
RP	MEDLINE; 97044477.
RA	Bonaldo M.F., Lennon G., Soares M.B.;
RX	"Normalization and subtraction: two approaches to facilitate gene
RT	discovery";
RL	Genome Res. 6(9):791-806(1996).
XX	
XX	UNILIB; 7287; 7287.
CC	Contact: Tuggle CK
CC	Molecular Genetics Laboratory, Department of Animal Science
CC	Iowa State University
CC	201 Kildee Hall, Ames, IA 50011-3150, USA
CC	Tel: 5152944252
CC	Fax: 5152942401
CC	Email: cktuggle@iastate.edu
CC	The sequence contained an oligo-dT track that was present in the
CC	oligonucleotide that was used to prime the synthesis of first
CC	strand cDNA and therefore this may represent a bonafide poly A
CC	tail. The sequence tag present in the cDNA between the NotI site
CC	and the oligo-dT track served to verify it as a clone from the
CC	normalized placenta library cDNA Library Preparation: M.B. Soares
CC	Lab, University of Iowa EST sequencing: M.B. Soares Lab, University
CC	of Iowa Clone Distribution: clones will be available through
CC	Research Genetics (www.resgen.com) The following repetitive
CC	elements were found in this cDNA sequence: 19-63,
CC	>POLY_A#Simple_repeat 295-321, >GC-rich#Low_complexity 461-484,
CC	>GC-rich#Low_complexity
CC	Seq primer: M13 Forward
CC	POLYA=Yes.
XX	
XX	Key Location/Qualifiers
PH	source
FT	1..576
FT	/db_xref=taxon:9823"
FT	/db_xref=UNILIB:7287"
FT	/note=Vector: pT73D-Pac (Pharmacia) with a modified
FT	polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-AV1
FT	library is normalized library derived from the MI-P-AV1
FT	library, ultimately derived from placenta tissue. For a
FT	detailed description of the library from which this clone
FT	was derived, please visit our web site at
FT	http://pigest.genome.iastate.edu/. The procedure used to
FT	create this library has been previously described (Bonaldo
FT	, Lennon and Soares, Genome Research 6: 791-806, 1996)
FT	TAG_LIB=MI-P-AV1 TAG_TISSUE=placenta TAG_SEQ=ATTG"
FT	/organism=Sus scrofa"
FT	/strain=Crossbred"
FT	/clone=MI-P-AV1-nqh-b-12-0-UI"
FT	/clone_lib=MI-P-AV1"
FT	/lab_host=DH10B (Life Technologies)"
XX	
SQ	Sequence 576 BP; 248 A; 119 C; 143 G; 66 T; 0 other;
	Query Match 1.4%; Score 29; DB 9; Length 576;
	Best Local Similarity 53.0%; Pred.No. 55;
	Matches 62; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY	1646 GTCATTTTATTATCTGTTATCGGTCTAAAGTCTAATTTACCACATTTTGATTTTCTGCTA 1705
Db	129 GTTTTTTTTTTTTGGTGGGGGTTAACCCCTGGGTTTTTTTTTAACTTTTAGGCC 70
QY	1706 GACAGATAACTTTTAATTTTCAAATTTGGCAGACACTTTTTTTTTTTTGTGAAAA 1762
Db	69 CCCCCCTTTTTTTTTTTTTTTTTTTCCTTTAAACAATTTTATTTTTTTTTTAAAAAA 13
RESULT 32	
HSM005765	
ID HSM005765	standard; RNA; EST; 130 BP.
XX	

2


```

DR UNILIB; 7286; 7286.
XX
CC Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized placenta library cDNA Library Preparation: M.B.
CC Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
CC University of Iowa Clone distribution: clones will be available
CC through Research Genetics (www.resgen.com)
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
FH Key Location/Qualifiers
FH source
FH 1. 197
FH /db_xref="taxon:9823"
FH /db_xref="UNILIB:7286"
FH /notes="Vector: pT73D-Pac (Pharmacia) with a modified
FH polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-Ay0
FH library is derived from placenta. For a detailed
FH description of the library from which this clone was
FH derived, please visit our web site at
FH http://pigest.genome.iastate.edu/. The procedure used to
FH create this library has been previously described (Bonaldo
FH , Lennon and Soares, Genome Research 6:791-806, 1996)
FH TAG_LIB=MI-P-Ay0 TAG_TISSUE=placenta TAG_SEQ=ATTGG"
FH /organism="Sus scrofa"
FH /clone="MI-P-Ay0-neu-h-08-0-UI"
FH /clone_lib="MI-P-Ay0"
FH /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 197 BP; 59 A; 58 C; 42 G; 38 T; 0 other;

Query Match 1.4%; Score 28.8; DB 9; Length 197;
Best Local Similarity 56.2%; Pred. No. 72;
Matches 54; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1853 GTGTGGAGGACTGGAGGTGCTTAGTCTGTTTCAGGTGCGGCATCTTGTGTTT 1912
Db 106 GGGTGGTGTGGAATAAAACCCGCTGAGGCTTGTGGGGGGGTGAGGTTTTCGCC 47
QY 1913 GCACATCTTTTAAATTTACACCTTTTCTTAAGAA 1948
Db 46 GGCCCCCTTTAAATTTTGTGCAAAAAA 11

RESULT 35
BF709877/c standard; RNA; EST; 313 BP.
XX
AC BF709877;
XX
SV BF709877.1
XX
DT 03-JAN-2001 (Rel. 66, Created)
DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX
DE MI-P-Ay1-npy-e-11-0-UI.s1 MI-P-Ay1 Sus scrofa cDNA clone
DE MI-P-Ay1-npy-e-11-0-UI 3', mRNA sequence.
XX
KW EST.
XX
OS Sus scrofa (pig)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

```

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OC Rutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
RN [1]
RP 1-313
RX MEDLINE: 97044477.
RA Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL discovery";
RL Genome Res. 6(9):791-806(1996).
XX
DR UNILIB; 7287; 7287.
XX
CC Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized placenta library cDNA Library Preparation: M.B. Soares
CC Lab, University of Iowa EST sequencing: M.B. Soares Lab, University
CC of Iowa Clone distribution: clones will be available through
CC Research Genetics (www.resgen.com) The following repetitive
CC elements were found in this cDNA sequence: 36-67,
CC >AT-rich#Low_complexity
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
FH Key Location/Qualifiers
FH source
FH 1. 313
FH /db_xref="taxon:9823"
FH /db_xref="UNILIB:7287"
FH /notes="Vector: pT73D-Pac (Pharmacia) with a modified
FH polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-Ay1
FH library is normalized library derived from the MI-P-Ay0
FH library, ultimately derived from placenta tissue. For a
FH detailed description of the library from which this clone
FH was derived, please visit our web site at
FH http://pigest.genome.iastate.edu/. The procedure used to
FH create this library has been previously described (Bonaldo
FH , Lennon and Soares, Genome Research 6: 791-806, 1996)
FH TAG_LIB=MI-P-Ay1 TAG_TISSUE=placenta TAG_SEQ=ATTGG"
FH /organism="Sus scrofa"
FH /strain="crossbreed"
FH /clone="MI-P-Ay1-npy-e-11-0-UI"
FH /clone_lib="MI-P-Ay1"
FH /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 313 BP; 118 A; 79 C; 59 G; 57 T; 0 other;

Query Match 1.4%; Score 28.8; DB 9; Length 313;
Best Local Similarity 60.0%; Pred. No. 66;
Matches 48; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1690 TTGTATTTTCTGCTAGACAGATAACTTTTAAATTTTCAATTTTGGCAGACACTTTTTT 1749
Db 107 TTCCTTTTTTTAGGAAAAAAATTCGCCGAATTCCTCCCTTTTTCGAAATTTTTTTT 48
QY 1750 TTTTGTGAAATCTTTTC 1769
Db 47 TTTTGTGAAATCTTTTC 28

RESULT 36
HSM010170 standard; RNA; EST; 115 BP.
XX

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AC AL045320;
XX
SV AL045320.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434A125_s1 (from clone DKFZp434A125)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-115
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No r1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FT source
FT 1. .115
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434A125"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 115 BP; 7 A; 9 C; 8 G; 90 T; 1 other;
Query Match 1.4%; Score 28.6; DB 2; Length 115;
Best Local Similarity 53.7%; Pred. No. 86;
Matches 58; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
OY 1286 CTTTGGCTTCTTGTGCTGATTTTCCCGAGATGAGTCTGCTATTTTGTACTTTTC 1345
DB 8 CTTTGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 67
OY 1346 TATGTATTATACTCTGAGAGTCACTAATAAGAGGAGTATTTT 1393
DB 68 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTAT 115
RESULT 37
HSM004384/c
ID HSM004384 standard; RNA; EST; 277 BP.
XX
AC AL039908;
XX
SV AL039908.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434H0112_s1 (from clone DKFZp434H0112)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
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XX
RN [1]
RP 1-277
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC r1 sequence also available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FT source
FT 1. .277
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434H0112"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 277 BP; 97 A; 45 C; 19 G; 114 T; 2 other;
Query Match 1.4%; Score 28.6; DB 2; Length 277;
Best Local Similarity 47.2%; Pred. No. 74;
Matches 85; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
OY 1613 AAAAGGTTAATGATTTTGTTCATTTCTGATTTGTTCATTTATCTGTTATCTGTTCTA 1672
DB 219 AAAAATGATGATTTCTGTTTGAAGAGAAGATAATTTTCTTTAGCGAGA 160
OY 1673 AAGTGTAAATTTACCATTTGATTTTCTGCTAGACAGATACTTTTAATTTTCAATT 1732
DB 159 GGTACAGTGTTTATATTTTGGAGCTTCTGAGGTGTAATAATTTGTAATAATTTATCT 100
OY 1733 TGGCAGACACTTTTCTTTTGTGAAAATCTTCTCCAGATCTGTGCCCACTGAA 1792
DB 99 NTGAGTAAATGTTAAGTAGTTGTTTAAATAACTTAATAAATAATTTCTTCTGTGGA 40
RESULT 38
BF703566
ID BF703566 standard; RNA; EST; 288 BP.
XX
AC BF703566;
XX
SV BF703566.1
XX
DT 26-DEC-2000 (Rel. 66, Created)
DT 26-DEC-2000 (Rel. 66, Last updated, Version 1)
XX
DE MI-P-H1-abl-a-03-1-UM.s1 MI-P-H1 Sus scrofa cDNA clone
DE MI-P-H1-abl-a-03-1-UM 3', mRNA sequence.
XX
KW EST.
XX
OS Sus scrofa (pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
RN [1]
RP 1-288
RX MEDLINE; 97044477.
RA Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL discovery";
RL Genome Res. 6(9):791-806(1996).
XX
```

DR UNILIB; 7279; 7279.
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142
CC Animal Science Research Center, Department of Animal Science,
CC University of Missouri-Columbia, 65211 Clone Distribution: clones
CC will be available through Research Genetics (www.resgen.com) The
CC following repetitive elements were found in this cDNA sequence:
CC 1-24, >AT_rich#Low_complexity 85-132, >POLY_A#Simple_repeat
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
FH Key Location/Qualifiers
FH source 1. .288
FT /db_xref="taxon:9823"
FT /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FT polylinker; Site_1: Not I; Site 2: EcoRI; The MI-P-H1
FT library is derived from hypothalamus at estrus day 0. For
FT a detailed description of the library from which this
FT clone was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. TAG_SEQ=None found"
FT /organism="Sus scrofa"
FT /strain="crossbreed"
FT /clone="MI-P-H1-abl-a-03-1-UM"
FT /clone_lib="MI-P-H1"
FT /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 288 BP; 111 A; 50 C; 7 G; 119 T; 1 other;

Query Match 1.4%; Score 28.6; DB 9; Length 288;
Best Local Similarity 51.1%; Pred.No. 73;
Matches 67; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1530 TTGCTTTTGTAGCAACATAAGAACCATGAGTCATTTTGTCTAGAGTATCTGTATAA 1589
Db 1 TTTTCTTTTATTAATAAATAAACAACACCTGTTTAAATTAACCTATTTTAA 60

QY 1590 AATCTCTGAAATCTGAATCAAAAGGTTAATGATTTTGTCTATCTGATTTGTC 1649
Db 61 AAAAACAATCTATTTTCAAAATAATTTATTTTATTTTTCCTCAATTTTAT 120

QY 1650 TTTTATTTATCT 1660
Db 121 TTTTATTTT 131

RESULT 39
BF704175/c standard; RNA; EST; 391 BP.
XX ID BF704175
AC BF704175;
XX SV BF704175.1
XX DT 26-DEC-2000 (Rel. 66, Created)
XX DT 26-DEC-2000 (Rel. 66, Last updated, Version 1)
XX MI-P-O3-aaw-c-12-1-UM.s1 MI-P-O3 Sus scrofa cDNA clone
DE MI-P-O3-aaw-c-12-1-UM 3', mRNA sequence.
XX EST.
XX

OS Sus scrofa (pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
RN 1-391
RX MEDLINE; 97044477.
RA Ronaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL Genome Res. 6(9):791-806(1996).
XX
XX UNILIB; 7285; 7285.
CC Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized ovary at estrus day 12 library cDNA library
CC Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science
CC Research Center, Department of Animal Science, University of
CC Missouri-Columbia, 65211 Clone Distribution: clones will be
CC available through Research Genetics (www.resgen.com)
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
FH Key Location/Qualifiers
FH source 1. .391
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7285"
FT /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FT polylinker; Site_1: Not I; Site 2: EcoRI; The MI-P-O3
FT library is derived from ovary at estrus day 12. For a
FT detailed description of the library from which this clone
FT was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. TAG_LIB=MI-P-O3
FT TAG_TISSUE=ovary at estrus day 12 TAG_SEQ=TTGTAC"
FT /organism="Sus scrofa"
FT /strain="crossbreed"
FT /clone="MI-P-O3-aaw-c-12-1-UM"
FT /clone_lib="MI-P-O3"
FT /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 391 BP; 155 A; 68 C; 89 G; 79 T; 0 other;

Query Match 1.4%; Score 28.6; DB 9; Length 391;
Best Local Similarity 52.0%; Pred.No. 69;
Matches 64; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1645 TGTCATTTTATATCTGTTATCGGTCTAAAGTGTCTAATTTACCATTTGTTCTGCT 1704
Db 151 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 92

QY 1705 AGACAGATAACTTTTAAATTTTCAAAATTTGGCAGACACTTTTTTTTTTTTTC 1764
Db 91 CCCCTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 32

QY 1765 TTT 1767
Db 31 TTT 29

RESULT 40
HSM001422/c

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ID HSM001422 standard; RNA; EST; 112 BP.
XX AC AL037097;
XX SV AL037097.1
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKF2p564L2264_r1 (from clone DKF2p564L2264)
XX KW EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX RN [1]
XX RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX RP 1-112
XX RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferpitz 10a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key Location/Qualifiers
XX FT source
XX FT 1. .112
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone="DKF2p564L2264"
XX FT /clone_lib="564 (synonym: hfr2). Vector pAMP1; host
XX FT x1-2blue; sites NotI + SalI"
XX FT /dev_stage="fetal"
XX FT /tissue_type="brain"
XX SQ Sequence 112 BP; 77 A; 4 C; 7 G; 2 T; 22 other;

Query Match 1.4%; Score 28.4; DB 2; Length 112;
Best Local Similarity 53.4%; Pred. No. 94;
Matches 47; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1682 TTACCATTTGATTTCTGCTAGACAGATAACTTTTAAATTTTCAAAATTTGGCAGACA 1741
Db 89 TTTTNCNTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30

QY 1742 CTTTTTTTTTTTTTTGAAATCTTCC 1769
Db 29 TTTTTTTTTTTTTTTTTTTTTTTTTTTCC 2

RESULT 41
BF703358/c
ID BF703358 standard; RNA; EST; 245 BP.
XX AC BF703358;
XX SV BF703358.1
XX 26-DEC-2000 (Rel. 66, Created)
DT 26-DEC-2000 (Rel. 66, Last updated, Version 1)
XX DE MI-P-O3-aav-a-12-1-UM.s1 MI-P-O3 Sus scrofa cDNA clone
XX DE MI-P-O3-aav-a-12-1-UM 3', mRNA sequence.
XX KW EST.

```

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OS Sus scrofa (pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX RN [1]
XX RP 1-245
XX RX MEDLINE; 97044477.
XX RA Bonaldo M.F., Lennon G., Soares M.B.;
XX RT "Normalization and subtraction: two approaches to facilitate gene
XX RL discovery";
XX RL Genome Res. 6(9):791-806(1996).
XX DR UNILIB; 7285; 7285.
XX CC Contact: Tuggle CK
XX CC Molecular Genetics Laboratory, Department of Animal Science
XX CC Iowa State University
XX CC 201 Kildee Hall, Ames, IA 50011-3150, USA
XX CC Tel: 5152944252
XX CC Fax: 5152942401
XX CC Email: cktuggle@iastate.edu
XX CC The sequence contained an oligo-dT track that was present in the
XX CC oligonucleotide that was used to prime the synthesis of first
XX CC strand cDNA and therefore this may represent a bonafide poly A
XX CC tail. The sequence tag present in the cDNA between the NotI site
XX CC and the oligo-dT track served to verify it as a clone from the
XX CC non-normalized ovary at estrus day 12 library cDNA Library
XX CC Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science
XX CC Research Center, Department of Animal Science, University of
XX CC Missouri-Columbia, 85211 Clone distribution: Clones will be
XX CC available through Research Genetics (www.resgen.com) the following
XX CC repetitive elements were found in this cDNA sequence: 1-23,
XX CC >AT rich#Low complexity 24-107, >POLY_A#Simple_repeat 201-232,
XX CC >GC_rich#Low complexity
XX CC Seq primer: M13 Forward
XX CC POLYA=yes.
XX FH Key Location/Qualifiers
XX FT source
XX FT 1. .245
XX FT /db_xref="taxon:9823"
XX FT /db_xref="UNILIB:7285"
XX FT /note="Vector: p7T3D-Pac (Pharmacia) with a modified
XX FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-O3
XX FT library is derived from ovary at estrus day 12. For a
XX FT detailed description of the library from which this clone
XX FT was derived, please visit our web site at
XX FT http://pigest.genome.iastate.edu/. TAG_LIB=MI-P-O3
XX FT TAG_TISSUE=ovary at estrus day 12 TAG_SEQ=TTGTAC"
XX FT /organism="Sus scrofa"
XX FT /strain="crossbred"
XX FT /clone_lib="MI-P-O3"
XX FT /clone_host="DH10B (Life Technologies)"
XX SQ Sequence 245 BP; 105 A; 59 C; 52 G; 29 T; 0 other;

Query Match 1.4%; Score 28.4; DB 9; Length 245;
Best Local Similarity 58.1%; Pred. No. 82;
Matches 50; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1686 CCATTTGATTTTCTGCTAGACAGATAACTTTTAAATTTTCAAAATTTGGCAGACTTT 1745
Db 109 CCTTTTTTTTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 24

QY 1746 TTTTTTTTTTTTGAATCTTCTTCTT 1771
Db 49 TTTTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 24

RESULT 42
BF708447
ID BF708447 standard; RNA; EST; 273 BP.

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XX AC BF708447;
 XX SV BF708447.1
 XX 03-JAN-2001 (Rel. 66, Created)
 XX 03-JAN-2001 (Rel. 66, Last updated, Version 1)
 XX MI-P-AY0-ncm-a-02-0-UI.s1 MI-P-AY0 Sus scrofa cDNA clone
 XX MI-P-AY0-ncm-a-02-0-UI 3', mRNA sequence.
 XX KW EST.
 XX Sus scrofa (pig)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 XX [1]
 XX MEDLINE; 97044477.
 XX 1-273
 RA Bonaldo M.F., Lennon G., Soares M.B.;
 RT "Normalization and subtraction: two approaches to facilitate gene
 RT discovery";
 RL Genome Res. 6(9):791-806(1996).
 XX UNILIB; 7286; 7286.
 XX Contact: Tuggle CK
 CC Molecular Genetics Laboratory, Department of Animal Science
 CC Iowa State University
 CC 201 Kildee Hall, Ames, IA 50011-3150, USA
 CC Tel: 515294252
 CC Fax: 5152942401
 CC Email: cktuggle@iastate.edu
 CC The sequence contained an oligo-dT track that was present in the
 CC oligonucleotide that was used to prime the synthesis of first
 CC strand cDNA and therefore this may represent a bonafide poly A
 CC tail. The sequence tag present in the cDNA between the NotI site
 CC and the oligo-dT track served to verify it as a clone from the
 CC non-normalized placenta library cDNA Library Preparation: M.B.
 CC Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
 CC University of Iowa Clone distribution: clones will be available
 CC through Research Genetics (www.resgen.com) The following repetitive
 CC elements were found in this cDNA sequence: 113-145,
 CC >AT_rich#Low_complexity 157-207, >AT_rich#Low_complexity
 CC Seq primer: M13 Forward
 CC POLYA=Yes.
 XX Key Location/Qualifiers
 FH source 1. 273
 FT /db_xref="taxon:9823"
 FT /db_xref="UNILIB:7286"
 FT /note="Vector: pT73D-Pac (Pharmacia) with a modified
 FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-AY0
 FT library is derived from placenta. For a detailed
 FT description of the library from which this clone was
 FT derived, please visit our web site at
 FT http://pigest.genome.iastate.edu/. The procedure used to
 FT create this library has been previously described (Bonaldo
 FT, Lennon and Soares, Genome Research 6:791-806, 1996)
 FT TAG LIB=MI-P-AY0 TAG TISSUE=placenta TAG_SEQ=ATTG"
 FT /organisms="Sus scrofa"
 FT /clone="MI-P-AY0-ncm-a-02-0-UI"
 FT /clone_lib="MI-P-AY0"
 FT /lab_hosts="DH10B (Life Technologies)"
 XX Sequence 273 BP; 118 A; 49 C; 48 G; 58 T; 0 other;
 Query Match 1.4%; Score 28.4; DB 9; Length 273;
 Best Local Similarity 50.0%; Pred. No. 80;
 Matches 71; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

. QY 1090 ATCTTCGACGACTTTGCTCACTAGGAGAGCGCCAGAGGAGGAGGTGTGTCGCAAGG 1149
 DB 62 AACCCCGGAAATTTTGGGAAAAAACAACAAACCCCAAGGGGGGAGGCCCAAAAAA 121
 QY 1150 AACGGCAGAGTCGAAACAACAATGAGGGGGAACCCAGTTTCTTACATGTTCTAACGTTTG 1209
 DB 122 AAAAAAATTTCTTAAAAAAGGGGGGCCAACCAATTAATAAATTTATTTATTTA 181
 QY 1210 ACTTTGAAAAACAGTTTAAAAACA 1231
 DB 182 AATAAAAAAATTTTAAAAA 203
 RESULT 43
 BM377646
 ID BM377646 standard; RNA; EST; 422 BP.
 XX AC BM377646;
 XX SV BM377646.1
 XX 15-JAN-2002 (Rel. 70, Created)
 XX 15-JAN-2002 (Rel. 70, Last updated, Version 1)
 XX EBem04 SQ003_M04_R IGF Barley EBem04 library Hordeum vulgare cDNA clone
 XX EBem04_SQ003_M04_5', mRNA sequence.
 XX EST.
 XX Hordeum vulgare
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 XX [1]
 RN Hedley P., Liu H., Caldwell D., McCallum N., Mudie S., Cardle L.,
 RA Ramsay L., Machray G., Marshall D.F.M., Waugh R.;
 RT "Development of Barley Transcriptome Resources";
 RL Unpublished.
 XX UNILIB; 9790; 9790.
 XX Contact: Waugh R
 CC Unit of Genomics
 CC Scottish Crop Research Institute
 CC Invergowrie, Dundee, DD2 5DA, Scotland, UK
 CC Tel: 00 44 1382 562731
 CC Fax: 00 44 1382 562426
 CC Email: tvaugh@scri.sari.ac.uk
 CC All sequence has a Phred quality score of 20 or over
 CC Seq primer: M13 reverse.
 XX Key Location/Qualifiers
 FH source 1. 422
 FT /db_xref="taxon:4513"
 FT /db_xref="UNILIB:9790"
 FT /note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
 FT Non-normalised library, directionally cloned into pSPORT1.
 FT Derived from embryos dissected from developing grains (12
 FT days post anthesis) in glasshouse grown barley plants.
 FT Developed as part of the barley transcriptome resources of
 FT BBSRC/SEERAD funded cereal IGF (Investigating Gene
 FT Function) project."
 FT /organism="Hordeum vulgare"
 FT /cultivar="Optic"
 FT /clone="EBem04_SQ003_M04"
 FT /clone_lib="IGF Barley EBem04 library"
 FT /tissue_type="Embryo"
 FT /dev_stage="12 days post anthesis"
 FT /lab_host="DH10B"

QY	1679	TAATTTACCATTTGATTTTCTGCTAGACAGATAAC	1715
Db	59	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	23
<p>Query Match 1.4%; Score 28.4; DB 6; Length 422; Best Local Similarity 50.0%; Pred. No. 74; Matches 71; Conservative 0; Mismatches 71; Indels 0; Gaps 0;</p>			
QY	675	CATCAAGAGTCTCTGAGACGACATCCACCGCTCATTAAAGTACTCCTCATCTGTTAG	734
Db	61	CACCAACGGCAGCGTCTGGGAACGACGACCAACGCGCCACCAAGAGAGGCGCTGCAGCTC	120
QY	735	CACAGAGCAGCGCAACAGCGCTGACGACGCGCTTCGCTCATGAGCAGCAAGGGGCC	794
Db	121	CATCAAGAACTGCTGTACTTCTCCGTCACGCGATCTTCGAGTCTCCTCATCAACGGCCT	180
QY	795	CGTCTACCTGCTCTTCAGGCTC 816	
Db	181	CTACCGCACCTCATGACGCC 202	
<p>RESULT 44 HSM011693/C ID HSM011693 standard; RNA; EST; 129 BP. XX AC AL046843; XX SV AL046843.1 XX DT 12-MAR-1999 (Rel. 59, Created) DT 12-MAR-1999 (Rel. 59, Last updated, Version 1) XX DE Homo sapiens mRNA; EST DKFZp586B0417_r1 (from clone DKFZp586B0417) XX KW EST; expressed sequence tag. XX OS Homo sapiens (human) OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; OC Eutheria; Primates; Catarrhini; Hominidae; Homo. XX RN [1] RP 1-129 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY XX CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA CC sequencing consortium of the German Genome Project CC No sl sequence available CC This clone is available at the RZPD in Berlin CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de XX RN [1] RP 1-129 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY XX CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA CC sequencing consortium of the German Genome Project CC No sl sequence available CC This clone is available at the RZPD in Berlin CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de XX RN [1] RP 1-129 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY XX CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA CC sequencing consortium of the German Genome Project CC No sl sequence available CC This clone is available at the RZPD in Berlin CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de XX RN [1] RP 1-129 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY XX CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA CC sequencing consortium of the German Genome Project CC No sl sequence available CC This clone is available at the RZPD in Berlin CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de XX RN [1] RP 1-129 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY XX CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA CC sequencing consortium of the German Genome Project CC No sl sequence available CC This clone is available at the RZPD in Berlin CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de XX RN [1] RP 1-129 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY XX CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA CC sequencing consortium of the German Genome Project CC No sl sequence available CC This clone is available at the RZPD in Berlin CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de XX RN [1] RP 1-129 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY XX CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA CC sequencing consortium of the German Genome Project CC No sl sequence available CC This clone is available at the RZPD in Berlin CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de XX RN [1] RP 1-129 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY XX CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA CC sequencing consortium of the German Genome Project CC No sl sequence available CC This clone is available at the RZPD in Berlin CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de XX RN [1] RP 1-129 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY XX CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA CC sequencing consortium of the German Genome Project CC No sl sequence available CC This clone is available at the RZPD in Berlin CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de XX RN [1] RP 1-129 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY XX CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA CC sequencing consortium of the German Genome Project CC No sl sequence available CC This clone is available at the RZPD in Berlin CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de XX RN [1] RP 1-129 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY XX CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA CC sequencing consortium of the German Genome Project CC No sl sequence available CC This clone is available at the RZPD in Berlin CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de XX RN [1] RP 1-129 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY XX CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA CC sequencing consortium of the German Genome Project CC No sl sequence available CC This clone is available at the RZPD in Berlin CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de XX RN [1] RP 1-129 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY XX CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA CC sequencing consortium of the German Genome Project CC No sl sequence available CC This clone is available at the RZPD in Berlin CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de XX RN [1] RP 1-129 RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY XX CC Clone from S. Wiemann, sequenced by BMFZ within the CDNA CC sequencing consortium of the German Genome Project CC No sl sequence available CC This clone is available at the RZPD in Berlin CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de XX RN [1] RP</p>			

CC	Fax: 5152942401
CC	Email: kctuggle@iastate.edu
CC	The sequence contained an oligo-dT track that was present in the
CC	oligonucleotide that was used to prime the synthesis of first
CC	strand cDNA and therefore this may represent a bonafide poly A
CC	tail. The sequence tag present in the cDNA between the NotI site
CC	and the oligo-dT track served to verify it as a clone from the
CC	non-normalized anterior pituitary at estrus day 0 library cDNA
CC	Library Preparation: RJ Woods, JA Green, RS Prather SI42 Animal
CC	Science Research Center, Department of Animal Science, University
CC	of Missouri-Columbia, 65211 Clone distribution: clones will be
CC	available through Research Genetics (www.resgen.com) The following
CC	repetitive elements were found in this cDNA sequence: 1-22,
CC	>AT_rich#Low_complexity 145-194, >GC_rich#Low_complexity
CC	Seq primer: M13 Forward
CC	POLYA=Yes.
XX	
XX	Key Location/Qualifiers
PH	
FT	1. .337
FT	/db_xref="taxon:9823"
FT	/db_xref="UNILIB:7271"
FT	/notes="Vector: pT773D-Pac (Pharmacia) with a modified
FT	polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-A1
FT	library is derived from anterior pituitary at estrus day 0.
FT	For a detailed description of the library from which this
FT	Clone was derived, please visit our web site at
FT	http://pigest.genome.iastate.edu/. TAG LIB=MI-P-A1
FT	TAG TISSUE=anterior pituitary at estrus day 0
FT	TAG_SEQ=TAAGCC"
FT	/organism="Sus scrofa"
FT	/strains="crossbred"
FT	/clone="MI-P-A1-aap-a-08-1-U"
FT	/clone_lib="MI-P-A1"
FT	/lab_host="DH10B (Life Technologies)"
XX	
SQ	Sequence 337 BP; 109 A; 117 C; 78 G; 33 T; 0 other;
	Query Match 1.4%; Score 27.8; DB 9; Length 337;
	Best Local Similarity 53.2%; Pred. No. 99;
	Matches 59; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Qy	932 TTTTGTGAAGATGTACCAATAACGAGTCGCGCATATCAGGCTGGAGATAACGACA 991
Db	1 TTTTGTGTATTTTAAAAAAGGCCCAACCTTAAATAGGGGGAAGGGGAAAAA 60
Qy	992 ACAACCGGTACAACTCCGGGACACCCAGGAGTGCCTTAGAAAAAG 1042
Db	61 AAAACCAAAACCCCAACCCCGCCCCCCCCCAAAAGGAAACCCCAAAAAG 111
RESULT 52	
HSC9743/C	
ID	HSC9743 standard; RNA; EST; 343 BP.
XX	
AC	C03974;
XX	
SV	C03974.1
XX	
DT	29-JUL-1996 (Rel. 48, Created)
DT	29-JUL-1996 (Rel. 48, Last updated, Version 1)
XX	
DE	Human Heart cDNA, clone 3NHC2509.
XX	
KW	EST(expressed sequence tag).
XX	
OS	Homo sapiens (human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC	Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX	
RN	[1]
RP	1-343
RA	Nakamura Y.;

```

RT ; Submitted (22-FEB-1996) to the EMBL/GenBank/DBJ databases.
RL Yusuke Nakamura, Institute of Medical Science, the University of Tokyo,
RL Laboratory of Molecular Medicine; 4-6-1, Shirokanedai, Minato-ku, Tokyo
RL 108, Japan (E-mail:yusuke@ims.u-tokyo.ac.jp, Tel:81-3-5449-5372,
RL Fax:81-3-5449-5433)
RL XX
RL [2]
RL RN
RL 1-343
RA Tanaka T., Ogiwara A., Uchiyama I., Takagi T., Yazaki Y., Nakamura Y.;
RA "Construction of a Normalized Directionally Cloned cDNA Library from Adult
RT Heart and Analysis of 3040 Clones by Partial Sequencing";
RL Genomics 35:231-235(1996).
RL XX
XX Key Location/Qualifiers
FH source 1. .343
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /dev_stage="Adult"
FT /tissue_type="Heart"
FT XX
XX SQ Sequence 343 BP; 113 A; 112 C; 21 G; 85 T; 12 other;

Query Match 1.4%; Score 27.8; DB 2; Length 343;
Best Local Similarity 56.8%; Pred.No.99;
Matches 50; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1824 GATTGGGCTGATGGTGTGGGGCATGATGTGTGGAGAACTGGAAGTGTCTTTAGGTCT 1883
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1884 GGTTCAGGTCGGGCATCTTTTGTGTT 1911
Db ||| |||| |||| |||| |||| |||| |||| ||||
QY 219 AGTTACTGGTTGACATGTTTGTGCT 192

RESULT 53
BM099974
ID ID BM099974 standard; RNA; EST; 460 BP.
XX AC BM099974;
XX SV BM099974.1
XX XX
XX 22-NOV-2001 (Rel. 69, Created)
XX 22-NOV-2001 (Rel. 69, Last updated, Version 1)
XX DE EBes01_SQ004_M22_R IGF Barley EBes01 library Hordeum vulgare cDNA clone
XX DE EBes01_SQ004_M22_5', mRNA sequence.
XX KW
XX EST.
XX OS Hordeum vulgare
XX Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
XX Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
XX Triticaceae; Hordeum.
XX [1]
XX RN
XX 1-460
RP Hedley P., Liu H., Caldwell D., McCallum N., Mudie S., Cardle L.,
RA Ramsay L., Machray G., Marshall D.F.M., Waugh R.;
RA "Development of Barley Transcriptome Resources";
RL Unpublished.
XX XX
XX UNILIB; 9804; 9804.
XX
XX Contact: Waugh R
XX Unit of Genomics
XX Scottish Crop Research Institute
XX Invergowrie, Dundee, DD2 5DA, Scotland, UK
XX Tel: 00 44 1382 562731
XX Fax: 00 44 1382 562426

```

Email: rvaugh@scri.sari.ac.uk
CC All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.

XX Key Location/Qualifiers

PH source

FT 1..460

FT /db_xref=taxon:4513"

FT /db_xref=UNILIB:9804"

FT /notes=Vector; pSPORTI; Site 1: Sal I; Site 2: Not I;

FT Non-normalised library, directionally cloned into pSPORTI.
Derived from embryo sacs dissected from developing grains
(4-6 days post anthesis) in glasshouse grown barley plants.
Developed as part of the barley transcriptome resources of
BBSRC/SERAD funded cereal IGF (Investigating Gene
Function) project."

FT /organism="Hordeum vulgare"

FT /cultivar="Optic"

FT /clone="EBes01_SQ004_M22"

FT /tissue_lib="IGF Barley EBes01 library"

FT /tissue_type="Embryo Sac"

FT /dev_stage="4-6 days post anthesis"

FT /lab_host="DH10B"

XX Sequence 460 BP; 101 A; 154 C; 125 G; 80 T; 0 other;

Query Match 1..4%; Score 27.8; DB 6; Length 460;
Best Local Similarity 48.4%; Pred. No. 93;
Matches 77; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 637 GAGTTTGAGTGAATCTGAAAACGGCGGTGTTCATTGCATCAAGACTCCTCAGGAC 696
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 98 GGTTTCGAGGCCACCAGGAGGTGCAGCACCGCATCGCATCCTCTCTCCAAGTCC 157

QY 697 GACATCCACCGCTCCATTAGTAGTACTCCTCCTGTGTAGACAGACGCGAACACGCGC 756
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 158 GTCAAGAACCCTCGAAGAGGTGTGCTCCGATCTCGTGAAGGGCCCCAAAGGAGACGCTC 217

QY 757 CTGCACAGCGCCTTCCGCTGCATGAGCAGCAGCGGCC 795
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 218 AGGTCAAGGCCCGCTCAGATGCCACCACAGTGCTC 256

RESULT 54
AU217241/c standard; RNA; EST; 716 BP.

XX AU217241

AC AU217241;

SV AU217241.1

DT 17-JUL-2001 (Rel. 68, Created)

DT 17-JUL-2001 (Rel. 68, Last updated, Version 1)

XX Caenorhabditis elegans cDNA clone:yk85lg12 : 3' end, single read.

EST (expressed sequence tag).

OS Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
Rhabditiidae; Peloderinae; Caenorhabditis.

[1]
Kohara Y.;
Submitted (10-JUL-2001) to the EMBL/GenBank/DDBJ databases.
Yuji Kohara, National Institute of Genetics, Genome Biology Lab.: 1111
Yata, Mishima, Shizuoka 411-8540, Japan [E-mail:ykohara@lab.nig.ac.jp,
Tel:81-559-81-6854, Fax:81-559-81-6855]

[2]
Kohara Y., Shin-i T., Thierry-Mieg J., Thierry-Mieg D., Suzuki Y.,

CC The sequence contained an oligo-dT track that was present in the
 CC oligonucleotide that was used to prime the synthesis of first
 CC strand cDNA and therefore this may represent a bonafide poly A
 CC tail. The sequence tag present in the cDNA between the NotI site
 CC and the oligo-dT track served to verify it as a clone from the
 CC normalized placenta library cDNA Library Preparation: M.B. Soares
 CC Lab, University of Iowa EST sequencing: M.B. Soares Lab, University
 CC of Iowa Clone Distribution: clones will be available through
 CC Research Genetics (www.resgen.com) The following repetitive
 CC elements were found in this cDNA sequence: 54-172,
 CC >POLY_A\$Simple_repeat 193-274, >POLY_A\$Simple_repeat
 CC Seq primer: M13 Forward
 CC POLYA=yes.

Key Location/Qualifiers
 FT 1. 522
 FT /db_xref="taxon:9823"
 FT /note="Vector: pT73D-Pac (Pharmacia) with a modified
 FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-A1
 FT library is normalized library derived from the MI-P-A1
 FT library, ultimately derived from placenta tissue. For a
 FT detailed description of the library from which this clone
 FT was derived, please visit our web site at
 FT http://piget.genome.iastate.edu/. The procedure used to
 FT create this library has been previously described (Bonaldo
 FT Lennon and Soares, Genome Research 6: 791-806, 1996)
 FT TAG_LIB=MI-P-A1 TAG_TISSUE=placenta TAG_SEQ=ATTGG"
 FT /organism="Sus scrofa"
 FT /strain="crossbred"
 FT /clone="MI-P-A1-ngh-a-08-0-UI"
 FT /clone_lib="MI-P-A1"
 FT /lab_host="DH10B (Life Technologies)"
 XX Sequence 522 BP; 255 A; 108 C; 85 G; 74 T; 0 other;

Query Match 1.4%; Score 27.6; DB 9; Length 522;
 Best Local Similarity 50.8%; Pred. No. 99;
 Matches 66; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1638 TCTGATTTGTCATTATATCTGTTATCGTCTAAAGTCTAATTTACCATTTGATTT 1697

Db 174 TATTTTTTTTCCCTTTTATTTTATTTTGAACCATGGGTAAATTTTATTTT 115

QY 1698 TTCTGCTAGACAGATACTTTTAAATTTTCAATTTGCGACACTTTT 1757

Db 114 GGTTTTTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 55

QY 1758 GAAATATCTTT 1767

Db 54 TGGGAATTTT 45

RESULT 60
 BM818575/c standard; RNA; EST; 569 BP.
 ID BM818575
 AC BM818575;
 SV BM818575.1
 XX 10-MAR-2002 (Rel. 71, Created)
 DT 10-MAR-2002 (Rel. 71, Last updated, Version 1)
 XX K-EST0085904 S21SNU520s1 Homo sapiens cDNA clone S21SNU520s1-4-F12 5', mRNA
 DE sequence.
 DE EST.

XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX 1-569
 RN Kim N.S., Hahn Y., Oh J.H., Lee J.Y., Ahn H.Y., Chu M.Y., Kim M.R.,
 RA Oh K.J., Cheong J.E., Sohn H.Y., Kim J.M., Park H.S., Kim Y.S.;
 RT "21C Frontier Korean EST Project 2001";
 RL Unpublished.
 XX UNILIB; 10325; 10325.
 CC Contact: Kim YS
 CC Genome Research Center
 CC Korea Research Institute of Bioscience & Biotechnology
 CC 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 CC Tel: +82-42-860-4470
 CC Fax: +82-42-860-4409
 CC Email: yongsung@mail.kribb.re.kr
 CC Place: 4 row; F column: 12
 CC High quality sequence stop: 569.

Key Location/Qualifiers
 FT 1. 569
 FT /db_xref="taxon:9606"
 FT /note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;
 FT Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 FT bacterial alkaline phosphatase (BAP) and then deacapped with
 FT tobacco acid pyrophosphatase (TAP). The deacapped intact
 FT mRNA was ligated with DNA-RNA linker including EcoR I site
 FT by treatment of T4 RNA ligase and the first strand cDNA was
 FT synthesized from oligo dT-selected mRNA by priming with
 FT dT-tailed vector. The dT-tailed vector was adjusted to have
 FT about 60nt. The cDNA vector was circularized with E. coli
 FT DNA ligase after digestion of EcoRI which site is also
 FT included in vector. An RNA strand converted to a DNA strand
 FT by Okayama-Berg method. The obtained cDNA vectors were used
 FT for transformation of competent cells E. coli Top10P' by
 FT electroporation method. The cDNA libraries constructed by
 FT this method are full-length enriched cDNA library. After
 FT analyzing and sequencing about 2,000 ~ 3,000 colonies in
 FT original cDNA library, the abundant cDNAs were selected and
 FT amplified by PCR reaction using vector region primer
 FT including T7 promotor as 5' primer and N(dt)14 as 3'
 FT primer. The PCR products were used as template for
 FT synthesis of biotinylated single stranded RNA by in vitro
 FT transcription reaction. The synthesized RNA probes were
 FT hybridized with antisense single stranded cDNAs prepared
 FT from original library and incubated with avidin-gel. After
 FT removing DNA-RNA hybrids by centrifuge, the subtracted cDNA
 FT libraries were constructed by transformation of the
 FT remaining DNA into competent cells E. coli Top10P' with
 FT electroporation method."

/sex="F"
 /organism="Homo sapiens"
 /clone="S21SNU520s1-4-F12"
 /clone_lib="S21SNU520s1"
 /tissue_type="Stomach"
 /cell_line="SNU-520"
 /lab_host="Top10P'"

XX Sequence 569 BP; 183 A; 122 C; 137 G; 127 T; 0 other;

Query Match 1.4%; Score 27.6; DB 2; Length 569;
 Best Local Similarity 49.3%; Pred. No. 98;
 Matches 72; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1626 TTTTGTTCATTCGATTTGTCATTTTATTTATCTGTTATCGTCTAAAGTCTGCTAATTTA 1685

Db 416 TTTTGTTCATTCGATTTGTCATTTTATTTTATTTTATTTTATTTTATTTTATTTT 357

QY 1686 CCCATTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGCGACACTTT 1745

```

Db 356 ATTAATAGCTGCAGTCTCAAAATCTTTTCATCATCAGATGTTGCGGAAGTTT 297
Qy 1746 TTTTTCATTTTGAATAATCTTTTCCTT 1771
Db 296 GGCCTTCTAGTGTGAACCTGGACCTT 271

RESULT 61
HSM012004
ID HSM012004 standard; RNA; EST; 647 BP.
AC AL047154;
XX AL047154.1
SV AL047154.1
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp586E2018_r1 (from clone DKFZp586E2018)
KW EST; expressed sequence tag.
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
RN 1-647
RA Wambutt R., Heubner D., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by AGOWA within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
PH Key Location/Qualifiers
FH source 1..647
FT /db xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp586E2018"
FT /clone_lib="586 (synonym: hutel). Vector pSport1; host
FT DH10B; sites NotI + SalI/MluI"
FT /dev_stage="adult"
FT /tissue_type="uterus"
XX
SQ Sequence 647 BP; 220 A; 94 C; 124 G; 206 T; 3 other;

Query Match 1..647
Best Local Similarity 1.4%; Score 27.6; DB 2; Length 647;
Matches 66; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 1557 TGAGTCTATTTGTCATTTAGAGTATCTTGATAAAATCTTTGAAAATCTCAAAATCAAAA 1616
Db 297 TCATCCATATCATACTTTATGACAGAGGAGGAGTGTGTTTAATCTTTGGAATTTAAAG 356

Qy 1617 GGTTAATGATTTTGTTCATTTCTGATTTGTCAATTTTATTTATCTGTTATCGGTCTAAAGT 1676
Db 357 ATTAACAAGTTTGGACAATATTGCTTTTATTTTAAATTTAAATTTGAAAATATAA 416

Qy 1677 GCTAATTAC 1686
Db 417 ATTAATAATAC 426

RESULT 62
HSM003964
ID HSM003964 standard; RNA; EST; 798 BP.
AC AL039488;
XX AL039488.1
SV AL039488.1
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp434A1311_s1 (from clone DKFZp434A1311)
KW EST; expressed sequence tag.
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
RN 1-798
RA Duysterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC r1 sequence also available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
PH Key Location/Qualifiers
FH source 1..798
FT /db xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434A1311"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 798 BP; 210 A; 200 C; 183 G; 202 T; 3 other;

Query Match 1..798
Best Local Similarity 63.6%; Pred. No. 92;
Matches 42; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 1570 CATTTAGAGTATTTCTGATAAAATCTTTGAAAATCTCAAAATCAAAAGTTAATGATTTT 1629
Db 145 CAAATTCAGTGTGTGAGAAAACCTGGTAACCATGCAGAAATTTTAAACATCTATGAATTT 204

Qy 1630 TTGTTTC 1635
Db 205 TTTTTC 210

RESULT 63
HSM001209/C
ID HSM001209 standard; RNA; EST; 125 BP.
AC AL036892;
XX AL036892.1
SV AL036892.1
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp564A1064_r1 (from clone DKFZp564A1064)
KW EST; expressed sequence tag.
XX Homo sapiens (human)
OS

```



```

CC Research Center, Department of Animal Science, University of
CC Missouri-Columbia, 65211 Clone distribution: clones will be
CC available through Research Genetics (www.resgen.com) The following
CC repetitive elements were found in this cDNA sequence: 1-46,
CC >AT-rich#Low complexity
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
XX
FH Key Location/Qualifiers
FH source 1. .380
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7285"
FT /notes="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-03
FT library is derived from ovary at estrus day 12. For a
FT detailed description of the library from which this clone
FT was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. TAG LIB=MI-P-03
FT TAG TISSUE=ovary at estrus day 12 TAG_SEQ=TTGTAC"
FT /organism="Sus scrofa"
FT /strain="crossbreed"
FT /clone_lib="MI-P-03-abc-e-02-1-UM"
FT /clone="MI-P-03"
FT /lab_hosts="DH10B (Life Technologies)"
XX
SQ Sequence 380 BP; 124 A; 50 C; 67 G; 139 T; 0 other;
Query Match 1.4%; Score 27.4; DB 9; Length 380;
Best Local Similarity 52.1%; Pred. No. 1.1e+02;
Matches 85; Conservative 0; Mismatches 76; Indels 2; Gaps 1;
QY 1391 TTTTGTGAGCTTATCAATCAGCATGATCTAATGTGMAATGTAAGTATCCTTAAAAACAAA 1450
DB 162 TATTTTCGTGTTTACTTTCAGTGCCTAAGGCCATATGCAATTAACATTAAGCCCAAG 103
QY 1451 GCATCTATTTTGGCAGAAATGTGTTCTTAAATTCAGTCATTTGATATCTGTGAGACTT 1510
DB 102 ACATGGATGTTTAAAGAAATTAATGTTTAA--CAGTTTCACTGATGCTTTCACACTA 45
QY 1511 CATATTCTCATCCCTTTATTCCTTTTATAGCAACATAGAAA 1553
DB 44 TTTTATTAATAAATCATATATTTGCTTAAAAAATAAAAAA 2
RESULT 66
BM372823/c standard; RNA; EST; 402 BP.
ID BM372823
AC BM372823;
XX BM372823.1
SV BM372823.1
XX
DT 16-JAN-2002 (Rel. 70, Created)
DT 16-JAN-2002 (Rel. 70, Last updated, Version 1)
XX
EBma04 SQ002_A22 R IGF Barley EBma04 library Hordeum vulgare cDNA clone
DE EBma04_SQ002_A22_5', mRNA sequence.
XX
XX EST.
XX
OS Hordeum vulgare
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
XX
XX [1]
RN Hedley P., Liu H., Caldwell D., McCallum N., Mudie S., Cardle L.,
RA Ramay L., Machray G., Marshall D.F.M., Waugh R.;
RT "Development of Barley Transcriptome Resources";
RL Unpublished.
XX

```

```

DR UNILIB; 10113; 10113.
XX
XX Contact: Waugh R
CC Unit of Genomics
CC Scottish Crop Research Institute
CC Invergowrie, Dundee, DD2 5DA, Scotland, UK
CC Tel: 00 44 1382 562731
CC Fax: 00 44 1382 562426
CC Email: rwaugh@scri.sari.ac.uk
CC All sequence has a Phred quality score of 20 or over
CC Seq primer: M13 reverse.
XX
XX Key Location/Qualifiers
FH source 1. .402
FT /db_xref="taxon:4513"
FT /db_xref="UNILIB:10113"
FT /notes="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
FT Non-normalised library, directionally cloned into pSPORT1.
FT Derived from maternal tissue dissected from developing
FT grains (10 days post anthesis) in glasshouse grown barley
FT plants. Developed as part of the barley transcriptome
FT resources of BSRG/SERAD funded cereal IGF (investigating
FT Gene Function) project."
FT /organism="Hordeum vulgare"
FT /cultivar="Optic"
FT /clone="EBma04 SQ002_A22"
FT /clone_lib="IGF Barley EBma04 library"
FT /tissue_type="Maternal tissue"
FT /dev_stage="10 days post anthesis"
FT /lab_host="DH10B"
XX
SQ Sequence 402 BP; 84 A; 117 C; 104 G; 97 T; 0 other;
Query Match 1.4%; Score 27.4; DB 6; Length 402;
Best Local Similarity 49.0%; Pred. No. 1.1e+02;
Matches 73; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 696 CGACATCCACCGCTCCATTAACTACTCCATCTGCTGTAGCACAGACGACGCAACAGCG 755
DB 174 CGGGCTCGTCCGCTGCAGGGGCATCCGACGTGGGGAGCATCGCCCTGTCTCTCTGCA 115
QY 756 CTGTGACAGCGCTTTCGCTGCATGACAGCAAGGGCCGCTCTACCTGTCTTTCAGCGT 815
DB 114 TCGAGCTTGATTTCAGCGGAGCATCGGCCCTGCGCCCTGTCAGCAGCCTCCATGGAGT 55
QY 816 CAATGGGAGTGGGCATTTTGTGGGTGG 844
DB 54 CGATGATCTCTCGATCCTCTTGAGTGC 26
RESULT 67
BM370203
ID BM370203 standard; RNA; EST; 437 BP.
XX
AC BM370203;
XX BM370203.1
SV BM370203.1
XX
DT 16-JAN-2002 (Rel. 70, Created)
DT 16-JAN-2002 (Rel. 70, Last updated, Version 1)
XX
EBro08 SQ003_E22 R IGF Barley EBro08 library Hordeum vulgare cDNA clone
DE EBro08_SQ003_E22_5', mRNA sequence.
XX
XX EST.
XX
OS Hordeum vulgare
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
XX
XX [1]
RN

```

RP 1-437 Hedley P., Liu H., Caldwell D., McCallum N., Mudie S., Cardle L.,
RA Ramsey L., Machray G., Marshall D.F.M., Waugh R.,
RT "Development of Barley Transcriptome Resources";
RL Unpublished.
XX
DR UNILIB; 9796; 9796.
XX
CC Contact: Waugh R
CC Unit of Genomics
CC Scottish Crop Research Institute
CC Invergowrie, Dundee, DD2 5DA, Scotland, UK
CC Tel: 00 44 1382 562731
CC Fax: 00 44 1382 562426
CC Email: rwaugh@scri.sari.ac.uk
CC All sequence has a Phred quality score of 20 or over
CC Seq primer: M13 reverse.
XX
FH Key Location/Qualifiers
FH
FT source
FT 1. .437 /db_xref="taxon:4513"
FT /db_xref="UNILIB:9796"
FT /note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
FT Non-normalised library, directionally cloned into pSPORT1.
FT Derived from roots of 3 week old drought stressed barley
FT plants. Developed as part of the barley transcriptome
FT resources of BSRG/SEERAD funded cereal IGF (Investigating
FT Gene Function) project."
FT /organism="Hordeum vulgare"
FT /cultivar="Optic"
FT /clone="EBro08_SQ003_E22"
FT /clone_lib="IGF Barley EBro08 library"
FT /tissue_type="Drought stressed root"
FT /lab_host="DH108"
XX
SQ Sequence 437 BP; 99 A; 111 C; 98 G; 129 T; 0 other;

Query Match 1.4%; Score 27.4; DB 6; Length 437;
Best Local Similarity 51.2%; Pred. No. 1.1e+02;
Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1657 ATCTGTATCGGTCTAAGTGCTAAATTTACCCATTTGATTTTCTGCTAGACAGATAACT 1716
DB 258 AGCCGTCATGATACATAGGAGTATCTCACCTTTTCTCTCTCTTTCTTCCAGCTTTCT 317
QY 1717 TTTAAATTTTCAAAATTTGGCAGACACTTTTATTTTGTGAAATCTTTCTTCCAGA 1776
DB 318 TCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 377
QY 1777 TCTGT 1781
DB 378 GCTGT 382

RESULT 68
BM854730/c standard; RNA; EST; 604 BP.
ID BM854730
XX
AC BM854730;
XX
SV BM854730.1
XX
DT 11-MAR-2002 (Rel. 71, Created)
DT 11-MAR-2002 (Rel. 71, Last updated, Version 1)
XX
K-EST0137384 S14K402 Homo sapiens cDNA clone S14K402-35-H10 5', mRNA
DE sequence.
DE
XX
KW EST.
XX
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-604
RA Kim N.S., Hahn Y., Oh J.H., Lee J.Y., Ahn H.Y., Chu M.Y., Kim M.R.,
RA Oh K.J., Cheong J.E., Sohn H.Y., Kim J.M., Park H.S., Kim S., Kim Y.S.;
RT "21C Frontier Korean EST Project 2001";
RL Unpublished.
XX
DR UNILIB; 10316; 10316.
XX
CC Contact: Kim YS
CC Genome Research Center
CC Korea Research Institute of Bioscience & Biotechnology
CC 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
CC Tel: +82-42-860-4470
CC Fax: +82-42-860-4409
CC Email: yongsung@mail.kribb.re.kr
CC Plate: 35 row: H column: 10
CC High quality sequence stop: 604.
XX
FH Key Location/Qualifiers
FH
FT source
FT 1. .604 /db_xref="taxon:9606"
FT /db_xref="UNILIB:10316"
FT /note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;
FT Site 2: NotI; The poly (A) + RNA was dephosphorylated with
FT bacterial alkaline phosphatase (BAP) and then decapped with
FT tobacco acid pyrophosphatase (TAP). The decapped intact
FT mRNA was ligated with DNA-RNA linker including EcoR I site
FT by treatment of T4 RNA ligase and the first strand cDNA was
FT synthesized from oligo dt-selected mRNA by priming with
FT dt-tailed vector. The dt-tailed vector was adjusted to have
FT about 60nt. The cDNA vector was circularized with E. coli
FT DNA ligase after digestion of EcoRI which site is also
FT included in vector. An RNA strand converted to a DNA strand
FT by Okayama-Berg method. The obtained cDNA vectors were used
FT for transformation of competent cells E. coli Top10⁸ by
FT electroporation method. The cDNA libraries constructed by
FT this method are full-length enriched cDNA library."
FT /organism="Homo sapiens"
FT /clone="S14K402-35-H10"
FT /clone_lib="S14K402"
FT /cell_lines="K402"
FT /lab_host="Top10⁸"
XX
SQ Sequence 604 BP; 170 A; 181 C; 148 G; 105 T; 0 other;

Query Match 1.4%; Score 27.4; DB 2; Length 604;
Best Local Similarity 57.6%; Pred. No. 1e+02;
Matches 49; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1711 ATAACTTTTAAATTTTCAAAATTTGGCAGACACTTTTATTTTGTGAAATCTTCTCT 1770
DB 499 ATTTTATTTTATTTTATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 440
QY 1771 TCCAGATCTGTTGCCCACTGAACAG 1795
DB 439 TTTTGAATCAGTTTTCAGGGGACAG 415

RESULT 69
HSM002724/c standard; RNA; EST; 680 BP.
ID HSM002724
XX
AC AL038379;
XX
SV AL038379.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 25-SEP-1999 (Rel. 61, Last updated, Version 3)
XX

```
DE Homo sapiens mRNA; EST DKFZp566M222_s1 (from clone DKFZp566M222)
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
OS
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX [1]
RN
RP 1-680
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RT Submitted (24-SEP-1999) to the EMBL/GenBank/DBJ databases.
RL
RL MIPS, Am Klopferstratz 18a, D-82152 Martinsried, GERMANY
XX
XX RZPD; DKFZp566M222; DKFZp566M222.
XX
XX This is the 3' sequence of the clone insert
CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC sequenced by MediGenomix within the cDNA sequencing consortium
CC of the German Genome Project.
CC ri sequence also available.
CC This clone is available at the RZPD in Berlin.
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
FH
FH source
FT 1. 680
FT /db_xref="taxon:9606"
FT /db_xref="RZPD:DKFZp566M222"
FT /organism="Homo sapiens"
FT /clone="DKFZp566M222"
FT /clone_lib="566 (synonym: hfk2d). Vector pAMP1; host
FT x1-2blue; sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="kidney"
XX
XX Sequence 680 BP; 253 A; 104 C; 99 G; 224 T; 0 other;
XX
XX Query Match 1.4%; Score 27.4; DB 2; Length 680;
XX Best Local Similarity 47.0%; Pred. No. 1e+02;
XX Matches 85; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
QY 1610 ATCAAGGCTTAAGTATTTTGGTTCATCTGATTTGCTGATTTATCTGTTATCGGT 1669
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 218 ATCCGAAGTCTTCTGTTGAATAGCAGTAAGTATTTCTCTTATAAAATTTTCATAGT 159
QY 1670 CTAAGTGCTAATTTACCATTTGATTTTCTGCTAGACAGATAACTTTTAATTTTCAA 1729
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 158 GTTATAATCTGTTATTTTGGAGCTATCTGATACTAATAATCTCTTATTTCTT 99
QY 1730 ATTGGCAGACACTTTTTTTTTTTTTTTTTTTTGAANAATCTTTCTCCAGATCTGTCGCCACT 1789
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 98 CTTTAAATGAATGTTTGATTTGTTTCTCAATCAATGAAGATCCAGCTCCAGGTCGCCACA 39
QY 1790 G 1790
DB |||
DB 38 G 38
XX
XX RESULT 70
XX BF703694/c
ID BF703694 standard; RNA; EST; 269 BP.
XX
XX BF703694;
XX AC
XX BF703694.1
XX SV
XX BF703694.1
XX
XX 26-DEC-2000 (Rel. 56, Created)
XX 26-DEC-2000 (Rel. 56, Last updated, Version 1)
XX
XX
```

```
DE MI-P-E4-abp-e-04-1-UM.s1 MI-P-E4 Sus scrofa cDNA clone
XX MI-P-E4-abp-e-04-1-UM 3', mRNA sequence.
XX EST.
XX
XX Sus scrofa (pig)
OS
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
XX [1]
RN
RP 1-269
RA MEDLINE; 97044477.
RA Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RT discovery";
RL Genome Res. 6(9):791-806(1996).
XX
XX UNILIB; 7276; 7276.
XX
XX Contact: Tuggle CK
XX Molecular Genetics Laboratory, Department of Animal Science
XX Iowa State University
XX 201 Kildee Hall, Ames, IA 50011-3150, USA
XX Tel: 5152944252
XX Fax: 5152942401
XX Email: cktuggle@iastate.edu
XX The sequence contained an oligo-dT track that was present in the
XX oligonucleotide that was used to prime the synthesis of first
XX strand cDNA and therefore this may represent a bonafide poly A
XX tail. The sequence tag present in the cDNA between the NotI site
XX and the oligo-dT track served to verify it as a clone from the
XX non-normalized embryo at gestational day 14 library cDNA library
XX Preparation: RJ Woods, JA Green, RS Prather SI42 Animal Science
XX Research Center, Department of Animal Science, University of
XX Missouri-Columbia, 65211 Clone distribution: clones will be
XX available through Research Genetics (www.resgen.com) The following
XX repetitive elements were found in this cDNA sequence: 1-59,
XX >AT rich#Low complexity 107-187, >POLY_A#Simple_repeat 188-224,
XX >GC rich#Low complexity
XX Seq primer: M13 Forward
XX POLYA=Yes.
XX
XX Key Location/Qualifiers
FH
FH source
FT 1. 269
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7276"
FT /notes="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-E4
FT library is derived from embryo at gestational day 14. For
FT a detailed description of the library from which this
FT clone was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. TAG_LIB=MI-P-E4
FT TAG_TISSUE=embryo at gestational day 14 TAG_SEQ=ACTCAC"
FT /organism="Sus scrofa"
FT /strain="crossbred"
FT /clone="MI-P-E4-abp-e-04-1-UM"
FT /clone_lib="MI-P-E4"
FT /lab_host="DH10B (Life Technologies)"
XX
XX Sequence 269 BP; 129 A; 71 C; 39 G; 30 T; 0 other;
XX
XX Query Match 1.3%; Score 27.2; DB 9; Length 269;
XX Best Local Similarity 52.7%; Pred. No. 1.3e+02;
XX Matches 59; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 1249 CCAGTGTGTCGCCGCGGGGGTTCAGTGTTCGATCTTTCCTTCGTTCGTTGATT 1308
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 213 CCGGGGTTTCGCCCGCCCCCGGGGGGTTTTTTTATTTTTTTTTTTTCTCTTTT 154
QY 1309 TTTGCCAGATGGAATCTGCATTTTATTTGTACTTTTCTATGATTATTAATCC 1360
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 153 TCCGGGGGGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGCC 102
```

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RESULT 71
HSC2714/c      standard; RNA; EST; 382 BP.
XX
XX C04271;
AC
XX
XX C04271.1
SV
XX
XX 29-JUL-1996 (Rel. 48, Created)
DT
XX 29-JUL-1996 (Rel. 48, Last updated, Version 1)
DT
XX
XX Human Heart cDNA, clone 3NH3039.
DE
XX
XX EST(expressed sequence tag).
KW
XX Homo sapiens (human)
OS
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC
XX Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX [1]
RN 1-382
RP Nakamura Y.;
RA
RT
RL Submitted (22-FEB-1996) to the EMBL/GenBank/DBJ databases.
RL Yusuke Nakamura, Institute of Medical Science, The University of Tokyo,
RL Laboratory of Molecular Medicine; 4-6-1, Shirokanedai, Minato-ku, Tokyo
RL 108, Japan (E-mail:Yusuke@ims.u-tokyo.ac.jp, Tel:81-3-5449-5372,
RL Fax:81-3-5449-5433)
XX
XX [2]
RN 1-382
RP Tanaka T., Ogiwara A., Uchiyama I., Takagi T., Yazaki Y., Nakamura Y.;
RA "Construction of a Normalized Directionally Cloned cDNA Library from Adult
RT Heart and Analysis of 3040 Clones by Partial Sequencing";
RL Genomics 35:231-235 (1996).
XX
XX Key Location/Qualifiers
FH
FH source 1..382
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /dev_stage="Adult"
FT /tissue_type="Heart"
XX
XX Sequence 382 BP; 128 A; 136 C; 22 G; 95 T; 1 other;
SQ
Query Match 1..382 Score 27.2; DB 2; Length 382;
Best Local Similarity 56.8%; Pred. No. 1.2e+02;
Matches 50; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 1824 GATTGGCTGGATGCTGGGCGATGATGCGAGGACTGGAAGTGTCTTGGTCT 1883
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
271 GATTCGGAGGATCCTATGTTGGTGGGCGCTTGTATGATTATGCGGCTGATTAGT 212
QY 1884 GGTTCCGGTGGGCGATCTTTTGTGTT 1911
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
211 AGTTACTGTTGAACATGTTGTTGCT 184

RESULT 72
AU218039/c
ID AU218039 standard; RNA; EST; 571 BP.
XX
XX AU218039;
AC
XX
XX AU218039.1
SV
XX
XX 17-JUL-2001 (Rel. 68, Created)
DT
XX 17-JUL-2001 (Rel. 68, Last updated, Version 1)
DT
XX
XX Caenorhabditis elegans cDNA clone:yk859c04 : 3' end, single read.
DE

```

```

XX EST (expressed sequence tag).
KW
XX Caenorhabditis elegans
OS
XX Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC
XX Rhabditidae; Peloderinae; Caenorhabditis.
XX
XX [1]
RN 1-571
RP Kohara Y.;
RA
RT Submitted (10-JUL-2001) to the EMBL/GenBank/DBJ databases.
RL Yuji Kohara, National Institute of Genetics, Genome Biology Lab.; 1111
RL Yata, Mishima, Shizuoka 411-8540, Japan (E-mail:ykohara@lab.nig.ac.jp,
RL Tel:81-559-81-6854, Fax:81-559-81-6855)
XX
XX [2]
RN Kohara Y., Shin-i T., Thierry-Mieg J., Thierry-Mieg D., Suzuki Y.,
RA Sugano S.;
RA "A complementary view of the C.elegans genome.";
RT Unpublished.
XX
XX UNILIB; 9634; 9634.
DR
XX
XX Key Location/Qualifiers
FH
FH source 1..571
FT /db_xref="taxon:6239"
FT /db_xref="UNILIB:9634"
FT /sequenced_mol="cDNA to mRNA"
FT /sex="Hermaphrodite"
FT /organism="Caenorhabditis elegans"
FT /clone_lib="unpublished oligo-capped cDNA library"
FT /dev_stage="L1"
FT /strain="N2"
FT /tissue_type="whole animal"
XX
XX Sequence 571 BP; 195 A; 123 C; 114 G; 138 T; 1 other;
SQ
Query Match 1..571 Score 27.2; DB 3; Length 571;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Matches 56; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 1881 TCTGGTTCAGGGTCGGGCATCTCTTCTGTTGTCACATCTTTTAAATTTTACACCTTT 1940
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
105 TTGATGAGTCTTTTGTGCTTTTAAAGAAATCTTTTATTATTATTTCCCAATTC 46
QY 1941 CTTAAGAAATCTAATGCCGCTTAAAGTTTATACCAATAAGCT 1985
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
45 CTTTCCATTTTCTTCGTCCTCAATTAATTTAAATAAAAAAANCT 1

RESULT 73
HSM010819
ID HSM010819 standard; RNA; EST; 125 BP.
XX
XX AL045969;
AC
XX
XX AL045969.1
SV
XX
XX 12-MAR-1999 (Rel. 59, Created)
DT
XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)
DT
XX
XX Homo sapiens mRNA; EST DKFZp434N226_s1 (from clone DKFZp434N226)
DE
XX
XX EST; expressed sequence tag.
KW
XX Homo sapiens (human)
OS
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC
XX Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX [1]
RN

```

RP 1-125
RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases:
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by BMFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC r1 sequence also available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1. .125
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp5660182"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 125 BP; 1 A; 4 C; 5 G; 113 T; 2 other;

Query Match 1.3%; Score 27; DB 2; Length 125;
Best Local Similarity 51.3%; Pred. No. 1.7e+02;
Matches 60; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 1626 TTTTGTGTCATTCGATTTCTCATTTTATTATCTGTTATCGGTCTAAAGTCTAAATTTA 1685
Db 7 TTTTGTGTCATTCGATTTCTCATTTTATTATCTGTTATCGGTCTAAAGTCTAAATTTA 66

Qy 1686 CCCATTGATTTTCTGCTACAGATACATTTTAAATTTTCAAAATTTGGCAGACAC 1742
Db 67 TTTTGTGTCATTCGATTTCTCATTTTATTATCTGTTATCGGTCTAAAGTCTAAATTTA 123

RESULT 74
HSM002746/C
ID HSM002746 standard; RNA; EST; 265 BP.
XX
AC AL038400;
SV AL038400.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 25-SEP-1999 (Rel. 61, Last updated, Version 3)
XX
DE Homo sapiens mRNA; EST DKFZp5660182_s1 (from clone DKFZp5660182)
XX
KW EST; expressed sequence tag.
XX
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-265
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (24-SEP-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a, D-82152 Martinsried, GERMANY
XX
DR RZPD; DKFZp5660182; DKFZp5660182.
XX
CC This is the 3' sequence of the clone insert
CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC sequenced by MediGenomix within the cDNA sequencing consortium
CC of the German Genome Project.
CC No r1 sequence available.

CC This clone is available at the RZPD in Berlin.
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1. .265
FT /db_xref="taxon:9606"
FT /db_xref="RZPD:DKFZp5660182"
FT /organism="Homo sapiens"
FT /clone="DKFZp5660182"
FT /clone_lib="566 (synonym: hfkid2). Vector pAMP1; host
FT X1-2blue; sites NotI + SalI"
FT /dev stage="fetal"
FT /tissue_type="kidney"
XX
SQ Sequence 265 BP; 101 A; 37 C; 21 G; 106 T; 0 other;

Query Match 1.3%; Score 27; DB 2; Length 265;
Best Local Similarity 49.6%; Pred. No. 1.4e+02;
Matches 69; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 1534 TTTTACCAACATAGAAACCATGAGTCATTTGTCTATTTAGATGATTTCTGATAAAATC 1593
Db 219 TTTTATAAGACTACTATACAACTACAGAGTTTATGATTTAAAGCTTCTAAAGCTTCTA 160

Qy 1594 TCTTGAATAACTGAAATCAAAAGGTTAATGATTTTTTGTTCATTTCTGATTTGTCAATTT 1653
Db 159 TGGTGCATTTGATATATATATATTTTAAAGGTTTCTATATGGGATTTTCTATTTA 100

Qy 1654 ATTATCTGTTATCGGTCTA 1672
Db 99 TGTAGTAAATATTGTTCTA 81

RESULT 75
BF703011/c
ID BF703011 standard; RNA; EST; 649 BP.
XX
AC BF703011;
SV BF703011.1
XX
DT 26-DEC-2000 (Rel. 66, Created)
DT 26-DEC-2000 (Rel. 66, Last updated, Version 1)
XX
DE MI-P-E5-abn-a-08-1-UM.s1 MI-P-E5 Sus scrofa cDNA clone
DE MI-P-E5-abn-a-08-1-UM 3', mRNA sequence.
XX
KW EST.
XX
OS Sus scrofa (pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
RN [1]
RP 1-649
RA MEDLINE; 97044477.
RA Ronaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RT discovery";
RL Genome Res. 6(9):791-806(1996).
XX
DR UNILIB; 7277; 7277.
XX
CC Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the


```
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="434" (synonym: htee3). Vector pSport1; host
FT DH10B; sites NotI + SalI
FT /dev_stage="adult"
FT /tissue_type="testis"
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SQ Sequence 128 BP; 20 A; 8 C; 9 G; 89 T; 2 other;

Query Match 1.3%; Score 26.8; DB 2; Length 128;
Best Local Similarity 54.2%; Pred. No. 1.8e+02;
Matches 52; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 1626 TTTTGTGTCATTCGATTCGATTTTATTCATTCGTCGTAAGTCAATTTA 1685
Db 27 TTTTGTGTCATTCGATTCGATTTTATTCATTCGTCGTCGTAAGTCAATTTA 86
Qy 1686 CCCATTTGATTTTCTGCTAGACAGATAACTTTTAA 1721
Db 87 TTTTGTGTCATTCGATTCGATTTTATTCATTCGTCGTCGTAAGTCAATTTA 122

RESULT 78
HSM001338/c
ID HSM001338 standard; RNA; EST; 139 BP.
XX
AC AL037014;
XX
SV AL037014.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp564G0964_r1 (from clone DKFZp564G0964)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-139
RA Duisterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Olgien within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de
XX
FH Key Location/Qualifiers
FT source 1..139
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="434" (synonym: htee3). Vector pSport1; host
FT DH10B; sites NotI + SalI
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 139 BP; 100 A; 9 C; 9 G; 5 T; 16 other;

Query Match 1.3%; Score 26.8; DB 2; Length 139;
Best Local Similarity 48.2%; Pred. No. 1.8e+02;
Matches 55; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

..
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Qy 1644 TTGTCATTTTATTCATTCGTCGTAAGTCTAATTTACCATTTGATTTTCTGC 1703
Db 126 TNNNTNATNNNTNGNGGTTGACNGTTNGNTAAATTTTCTTTTCTTTT 67
Qy 1704 TAGACAGATAACTTTTAAATTTTCAAAATTTGGCAGACACTTTTCTTTT 1757
Db 66 TTTTGTGTCATTCGATTCGATTTTATTCATTCGTCGTCGTAAGTCAATTTA 13

RESULT 79
HSM002744
ID HSM002744 standard; RNA; EST; 147 BP.
XX
AC AL038398;
XX
SV AL038398.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp566O122_s1 (from clone DKFZp566O122)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-147
RA Ottenwaelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by MediGenomix within the cDNA
CC sequencing consortium of the German Genome Project
CC No r1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de
XX
FH Key Location/Qualifiers
FT source 1..147
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="566" (synonym: hfkd2). Vector pAMP1; host
FT X1-2blue; sites NotI + SalI
FT /dev_stage="fetal"
FT /tissue_type="kidney"
XX
SQ Sequence 147 BP; 4 A; 10 C; 10 G; 115 T; 8 other;

Query Match 1.3%; Score 26.8; DB 2; Length 147;
Best Local Similarity 52.7%; Pred. No. 1.8e+02;
Matches 58; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 1626 TTTTGTGTCATTCGATTTGTCATTTTATTCATTCGTCGTCGTAAGTCAATTTA 1685
Db 1 TTTTGTGTCATTCGATTTGTCATTTTATTCATTCGTCGTCGTAAGTCAATTTA 60
Qy 1686 CCCATTTGATTTTCTGCTAGACAGATAACTTTTAAATTTTCAAAATTTGG 1735
Db 61 TTTTGTGTCATTCGATTTGTCATTTTATTCATTCGTCGTCGTAAGTCAATTTA 110

RESULT 80
BF703629
ID BF703629 standard; RNA; EST; 224 BP.
XX
AC BF703629;
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[illegible]

QY 1679 TAATTACCATTTGATTTCTGCTAGACAGATAACTTTTAAATTTTCAAAATTTGGCAG 1738
 Db 69 TTTATTGCATAGAAATACACTGCTATTAATAATAATGCAATGTAATTTTATTTTGT 128
 QY 1739 ACACATTTTCTTTTCTTTTGAATACTTTTC 1768
 Db 129 TGTATTATTATTATTTTGGACACAGACTCTC 158

RESULT 84
 BF711270/c standard; RNA; EST; 469 BP.

XX AC BF711270;
 XX BF711270.1
 XX 03-JAN-2001 (Rel. 66, Created)
 DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
 DE MI-P-03-abb-C-12-1-UM.s1 MI-P-03 Sus scrofa cDNA clone
 DE MI-P-03-abb-C-12-1-UM 3', mRNA sequence.
 XX EST.

XX Sus scrofa (pig)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

XX [1]
 RN 1-469
 RP MEDLINE; 97044477.
 RA Bonaldo M.F., Lennon G., Soares M.B.;
 RX "Normalization and subtraction: two approaches to facilitate gene
 RT discovery";
 RL Genome Res. 6(9):791-806(1996).
 XX UNILIB; 7285; 7285.

XX Contact: Tuggle CK
 CC Molecular Genetics Laboratory, Department of Animal Science
 CC Iowa State University
 CC 201 Kildee Hall, Ames, IA 50011-3150, USA
 CC Tel: 5152944252
 CC Fax: 5152942401
 CC Email: cktuggle@iastate.edu

CC The sequence contained an oligo-dT track that was present in the
 CC oligonucleotide that was used to prime the synthesis of first
 CC strand cDNA and therefore this may represent a bonafide poly A
 CC tail. The sequence tag present in the cDNA between the NotI site
 CC and the oligo-dT track served to verify it as a clone from the
 CC non-normalized ovary at estrus day 12 library cDNA library
 CC Preparation: RJ Woods, JA Green, RS Prather SI42 Animal Science
 CC Research Center, Department of Animal Science, University of
 CC Missouri-Columbia, 65211 Clone distribution: clones will be
 CC available through Research Genetics (www.resgen.com) The following
 CC repetitive elements were found in this cDNA sequence: 155-191,
 CC >AT-rich#Low complexity
 CC Seq primer: M13 Forward
 CC POLVA=Yes.

XX Key Location/Qualifiers
 FH 1..469
 FH /db_xref="taxon:9823"
 FT /db_xref="UNILIB:7285"
 FT /note="Vector: pTZ19D-Pac (Pharmacia) with a modified
 FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-03
 FT library is derived from ovary at estrus day 12. For a
 FT detailed description of the library from which this clone
 FT was derived, please visit our web site at
 FT http://pigest.genome.iastate.edu/. TAG LIB=MI-P-03

FT TAG_TISSUE=ovary at estrus day 12 TAG_SEQ=TTGTAC"
 FT /organism="Sus scrofa"
 FT /strain="crossbreed"
 FT /clone="MI-P-03-abb-C-12-1-UM"
 FT /clone.lib="MI-P-03"
 FT /lab_host="DH10B (Life Technologies)"
 XX Sequence 469 BP; 181 A; 122 C; 76 G; 90 T; 0 other;

Query Match 1.3%; Score 26.8; DB 9; Length 469;
 Best Local Similarity 55.3%; Pred. No. 1.4e+02;
 Matches 52; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1690 TTTGATTTTCTGCTAGACAGATAACTTTTAAATTTTCAAAATTTGGCAGACACTTTT 1749
 Db 244 TTGGAATTTGGGGCTTTTGGGGAACCATTAATTTGGTTAAGTTGGATTACAAATTTT 185

QY 1750 TTTTGTGAAAATCTTTCCTTCCAGATCTGTTG 1783
 Db 184 TTGATTTTAAATTTTGTGAAAATTTGTTG 151

RESULT 85
 BM856410 standard; RNA; EST; 498 BP.

XX BM856410;
 XX BM856410.1
 XX 11-MAR-2002 (Rel. 71, Created)
 DT 11-MAR-2002 (Rel. 71, Last updated, Version 1)
 DE K-EST0140366 S14K402 Homo sapiens cDNA clone S14K402-48-A12 5', mRNA
 DE sequence.
 XX EST.

XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]
 RN 1-498
 RA Kim N.S., Hahn Y., Oh J.H., Lee J.Y., Ahn H.Y., Chu M.Y., Kim M.R.,
 RA Oh K.J., Cheong J.E., Sohn H.Y., Kim J.M., Park H.S., Kim S., Kim Y.S.;
 RT "21C Frontier Korean EST Project 2001";
 RL Unpublished.

XX UNILIB; 10316; 10316.

XX Contact: Kim YS
 CC Genome Research Center
 CC Korea Research Institute of Bioscience & Biotechnology
 CC 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 CC Tel: +82-42-860-4470
 CC Fax: +82-42-860-4409
 CC Email: yongsung@mail.kribb.re.kr
 CC Plate: 48 row: A column: 12
 CC High quality sequence stop: 498.

XX Key Location/Qualifiers
 FH 1..498
 FH /db_xref="taxon:9606"
 FT /db_xref="UNILIB:10316"
 FT /note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;
 FT Site 2: NotI; The poly (A) + RNA was dephosphorylated with
 FT bacterial alkaline phosphatase (BAP) and then deapped with
 FT tabacco acid pyrophosphatase (TAP). The deapped intact
 FT mRNA was ligated with DNA-RNA linker including EcoR I site
 FT by treatment of T4 RNA ligase and the first strand cDNA was
 FT synthesized from oligo dt-selected mRNA by priming with

FT dt-tailed vector. The dt-tailed vector was adjusted to have
FT about 60nt. The cDNA vector was circularized with E. coli
FT DNA ligase after digestion of EcoRI which site is also
FT included in vector. An RNA strand converted to a DNA strand
FT by Okayama-Berg method. The obtained cDNA vectors were used
FT for transformation of competent cells E. coli Top10p, by
FT electroporation method. The cDNA libraries constructed by
FT this method are full-length enriched cDNA library."
FT /organism="Homo sapiens"
FT /clone_lib="S14K402-48-A12"
FT /clone="S14K402"
FT /cell_line="K402"
FT /lab_host="Top10p."
XX

SQ Sequence 498 BP; 197 A; 81 C; 69 G; 151 T; 0 other;

Query Match 1.3%; Score 26.8; DB 2; Length 498;
Best Local Similarity 44.1%; Pred. No. 1.4e+02;
Matches 112; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY 1393 TTGTCAGCTTATCAATCAGACTGATCTAATGTAATGTAAGTATCCTTAAAAACAAGC 1452

DB 52 TTCTGACATAATCCAGTAAATATAATATTTTAAAGAAATAAATTTATTTCAATATTACCA 111

QY 1453 ATCTATTTTGGCAGAAATGTTCTTAAATTCAGTCAATTTGATATCTGTGAGACTTCA 1512

DB 112 AGACAGCATGCTTCAATCAATCTGTAATACTGAAGAACTTAAATTTTGTCTTACTG 171

QY 1513 TATTTTCATCCCTTTATGCTTTTGTAGCAACATAGAAACCATGATCTTTTGTGAT 1572

DB 172 CTTAATTCAAATAATAATTTGCTAGCAATAGTAATCTGTAAGCATTAAGCTTATGCTTAAA 231

QY 1573 TTACGATATCTCGATAAATCTTTGAAATCTGAAATCAAAAGGTTAATGATTTTTTG 1632

DB 232 TTCAGTTTATGTTGAGGAATCTTTAAATATACAACTAAGTATGTTGTATGCTATTTT 291

QY 1633 TTCATTCTGATTTG 1646

DB 292 TTTCAGTTTATTTG 305

RESULT 86

HS0004754
ID HSM004754 standard; RNA; EST; 110 BP.

AC AL040278;

SV AL040278.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp34K2413_s1 (from clone DKFZp34K2413)

XX EST; expressed sequence tag.

XX Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]

RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPPS, Am Klopferstritz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by BMFZ within the cDNA

CC sequencing consortium of the German Genome Project

CC cl sequence also available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers
FH source 1. 110
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_lib="DKFZp34K2413"
FT /clone_lib="434 (synonym: htes3). Vector p9port1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX

SQ Sequence 110 BP; 11 A; 4 C; 4 G; 91 T; 0 other;

Query Match 1.3%; Score 26.6; DB 2; Length 110;
Best Local Similarity 54.6%; Pred. No. 2e+02;
Matches 53; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1626 TTTTGTTCATCTCGATTTGTCATTTTATTTATCTGTTATCGTCTAAAGTGCTAATTTA 1685

DB 1 TTTTGTTCATCTCGATTTGTCATTTTATTTATCTGTTATCGTCTAAAGTGCTAATTTA 60

QY 1686 CCCATTTGATTTTCTGCTAGACAGATACTTTAAT 1722

DB 61 TTTTGTTCATCTCGATTTGTCATTTTATTTATCTGTTATCGTCTAATTTAAT 97

RESULT 87

BF702532/c
ID BF702532 standard; RNA; EST; 124 BP.

AC BF702532;

SV BF702532.1

DT 25-DEC-2000 (Rel. 66, Created)

DT 25-DEC-2000 (Rel. 66, Last updated, Version 1)

DE MI-P-E3-aak-d-10-1-UM s1 MI-P-E3 Sus scrofa cDNA clone

DE MI-P-E3-aak-d-10-1-UM 3', mRNA sequence.

XX EST.

XX Sus scrofa (pig)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

XX [1]

RP 1-124

RX MEDLINE; 97044477.

RA Bonaldo M.F., Lennon G., Soares M.B.;

RT "Normalization and subtraction: two approaches to facilitate gene

RL Genome Res. 6(9):791-806(1996).

XX UNILIB; 7275; 7275.

CC Contact: Tuggle CK

CC Molecular Genetics Laboratory, Department of Animal Science

CC Iowa State University

CC 201 Kildee Hall, Ames, IA 50011-3150, USA

CC Tel: 5152944252

CC Fax: 5152942401

CC Email: ktuggle@iastate.edu

CC The sequence contained an oligo-dT track that was present in the

CC oligonucleotide that was used to prime the synthesis of first

CC strand cDNA and therefore this may represent a bonafide poly A

CC tail. The sequence tag present in the cDNA between the NotI site

CC and the oligo-dT track served to verify it as a clone from the

CC non-normalized fetus at gestational day 45 library cDNA library

CC Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science

CC Research Center, Department of Animal Science, University of

CC Missouri-Columbia, 65211 Clone distribution: clones will be

available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 13-123, >POLY A#Simple repeat
 Seq primer: M13 Forward
 POLYA=yes.

Key Location/Qualifiers
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 /db_xref="taxon:9823"
 /db_xref="UNILIB:7275"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: EcoRI; The MI-P-E3 library is derived from fetus at gestational day 45. For a detailed description of the library from which this clone was derived, please visit our web site at http://pigest.genome.iastate.edu/. TAG LIB=MI-P-E3 TAG_TISSUE=fetus at gestational day 45 TAG_SEQ=CGCGAC"
 /organism="Sus scrofa"
 /strain="crossbreed"
 /clone="MI-P-E3-aak-d-10-1-UM"
 /clone_lib="MI-P-E3"
 /lab_host="DH10B (Life Technologies)"

Sequence 124 BP; 110 A; 0 C; 1 G; 13 T; 0 other;

Query Match 1.3%; Score 26.6; DB 9; Length 124;
 Best Local Similarity 52.2%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 59; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 1650 TTTTATTATCTGTATCGGTCTAAAGTCTAAATTTACCCATTGATTTCTCTAGACA 1709
 |||||
 DB 121 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 62
 |||||
 QY 1710 GATACTTTTAAATTTTCAAAATTTGGCAGACATTTTATTTTGTGAAA 1762
 |||||
 DB 61 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 9
 |||||

RESULT 89
 HSM010835
 ID HSM010835 standard; RNA; EST; 127 BP.
 XX
 AC AL045985;
 XX
 SV AL045985.1
 XX
 DT 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX
 DE Homo sapiens mRNA; EST DKFZp4340136_s1 (from clone DKFZp4340136)
 XX
 KW EST; expressed sequence tag.
 XX
 OS Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX
 RN [1]
 RP Koehler K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
 RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY
 XX
 CC Clone from S. Wiemann, sequenced by BMPZ within the cDNA
 CC sequencing consortium of the German Genome Project
 CC ri sequence also available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 XX
 XX Key Location/Qualifiers

FH source 1..127
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp4340136"
 FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX
 SQ Sequence 127 BP; 3 A; 3 C; 6 G; 112 T; 3 other;

Query Match 1.3%; Score 26.6; DB 2; Length 127;
 Best Local Similarity 51.3%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 59; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1644 TTGTCAATTTTATCTGTATCGGTCTAAAGTCTAAATTTACCCATTGATTTCTGCG 1703
 |||||
 DB 1 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 60
 |||||
 QY 1704 TAGACAGATAACTTTTAAATTTTCAAAATTTGGCAGACATTTTATTTTGTG 1758
 |||||
 DB 61 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 115
 |||||

RESULT 89
 BF703980/c
 ID BF703980 standard; RNA; EST; 217 BP.
 XX
 AC BF703980;
 XX
 SV BF703980.1
 XX
 DT 26-DEC-2000 (Rel. 66, Created)
 DT 26-DEC-2000 (Rel. 66, Last updated, Version 1)
 XX
 DE MI-P-O1-abe-h-02-1-UM.s1 MI-P-O1 Sus scrofa cDNA clone
 DE MI-P-O1-abe-h-02-1-UM 3', mRNA sequence.
 XX
 KW EST.
 XX
 OS Sus scrofa (pig)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 XX
 RN [1]
 RP 1-217
 RX MEDLINE; 97044477.
 RA Ronaldo M.F., Lennon G., Soares M.B.;
 RT "Normalization and subtraction: two approaches to facilitate gene
 RT discovery";
 RL Genome Res. 6(9):791-806(1996).
 XX
 DR UNILIB; 7283; 7283.
 XX
 CC Contact: Tuggle CK
 CC Molecular Genetics Laboratory, Department of Animal Science
 CC Iowa State University
 CC 201 Kildee Hall, Ames, IA 50011-3150, USA
 CC Tel: 5152944252
 CC Fax: 5152942401
 CC Email: cktuggle@iastate.edu
 CC The sequence contained an oligo-dT track that was present in the
 CC oligonucleotide that was used to prime the synthesis of first
 CC strand cDNA and therefore this may represent a bonafide poly A
 CC tail. The sequence tag present in the cDNA between the NotI site
 CC and the oligo-dT track served to verify it as a clone from the
 CC non-normalized ovary at estrus day 0 library cDNA library
 CC Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science
 CC Research Center, Department of Animal Science, University of
 CC Missouri-Columbia, 65211 Clone distribution: clones will be
 CC available through Research Genetics (www.resgen.com) The following
 CC repetitive elements were found in this cDNA sequence: 1-27,


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OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
RN 1-300
RX MEDLINE; 97044477.
RA Ronaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL discovery";
RL Genome Res. 6(9):791-806(1996).
XX
XX
XX UNILIB; 7286; 7286.
DR
XX
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized placenta library cDNA library Preparation: M.B.
CC Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
CC University of Iowa Clone distribution: clones will be available
CC through Research Genetics (www.resgen.com) The following repetitive
CC elements were found in this cDNA sequence: 1-99,
CC >POLY_A$Simple_repeat 221-252, >GC_rich$Low_complexity
CC Seq primer: Mi3 Forward
CC POLYA=Yes.
XX
XX Key Location/Qualifiers
FH source
FH 1..300
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7286"
FT /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-Ay0
FT library is derived from placenta. For a detailed
FT description of the library from which this clone was
FT derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. The procedure used to
FT create this library has been previously described (Bonaldo
FT , Lennon and Soares, Genome Research 6:791-806, 1996)
FT TAG_LIB=MI-P-Ay0 TAG_TISSUE=placenta TAG_SEQ=ATTGG"
FT /organism="Sus scrofa"
FT /clone="MI-P-Ay0-nev-a-09-0-UI"
FT /clone_lib="MI-P-Ay0"
FT /lab_host="DH10B (Life Technologies)"
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Query Match 1.3%; Score 26.6; DB 9; Length 300;
Best Local Similarity 52.2%; Pred. No. 1.7e+02;
Matches 59; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
QY 1690 TTGATTTTCTGTAGACAGATACCTTTTAAATTTTCAATTTGGCAGACACTTTTTT 1749
Db 2 TTTTTTTTTTTTTTTTGGTCTCCCTTTTTTTTTTTTTTAAATTTTTTTTTTTTTTTT 61
QY 1750 TTTTGTGAAATCTTCTCCAGATCTGTGCCACTGACAGACCCCG 1802
Db 62 TTATTTTTTTTTTTTTTTTATTTATTTTATTTTCTTACCCCCCTCCCG 114
RESULT 92
BF710556/c standard; RNA; EST; 346 BP.
XX
XX AC BF710556;
XX
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SV BF710556.1
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XX 03-JAN-2001 (Rel. 66, Created)
XX 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX
XX MI-P-Ay1-nre-e-10-0-UI-s1 MI-P-Ay1 Sus scrofa cDNA clone
XX MI-P-Ay1-nre-e-10-0-UI 3', mRNA sequence.
XX EST.
XX
XX Sus scrofa (pig)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
XX 1-346
XX MEDLINE; 97044477.
XX Ronaldo M.F., Lennon G., Soares M.B.;
XX "Normalization and subtraction: two approaches to facilitate gene
XX discovery";
XX Genome Res. 6(9):791-806(1996).
XX UNILIB; 7287; 7287.
XX
XX Contact: Tuggle CK
XX Molecular Genetics Laboratory, Department of Animal Science
XX Iowa State University
XX 201 Kildee Hall, Ames, IA 50011-3150, USA
XX Tel: 5152944252
XX Fax: 5152942401
XX Email: cktuggle@iastate.edu
XX The sequence contained an oligo-dT track that was present in the
XX oligonucleotide that was used to prime the synthesis of first
XX strand cDNA and therefore this may represent a bonafide poly A
XX tail. The sequence tag present in the cDNA between the NotI site
XX and the oligo-dT track served to verify it as a clone from the
XX non-normalized placenta library cDNA library Preparation: M.B. Soares
XX Lab, University of Iowa EST sequencing: M.B. Soares Lab, University
XX of Iowa Clone distribution: clones will be available through
XX Research Genetics (www.resgen.com) The following repetitive
XX elements were found in this cDNA sequence: 63-175,
XX >POLY_A$Simple_repeat
XX Seq primer: Mi3 Forward
XX POLYA=Yes.
XX
XX Key Location/Qualifiers
FH source
FH 1..346
FH /db_xref="taxon:9823"
FH /db_xref="UNILIB:7287"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-Ay1
FH library is normalized library derived from the MI-P-Ay0
FH library, ultimately derived from placenta tissue. For a
FH detailed description of the library from which this clone
FH was derived, please visit our web site at
FH http://pigest.genome.iastate.edu/. The procedure used to
FH create this library has been previously described (Bonaldo
FH , Lennon and Soares, Genome Research 6:791-806, 1996)
FH TAG_LIB=MI-P-Ay1 TAG_TISSUE=placenta TAG_SEQ=ATTGG"
FH /organism="Sus scrofa"
FH /strains="crossbreed"
FH /clone="MI-P-Ay1-nre-e-10-0-UI"
FH /clone_lib="MI-P-Ay1"
FH /lab_host="DH10B (Life Technologies)"
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XX Sequence 346 BP; 180 A; 52 C; 55 G; 59 T; 0 other;
Query Match 1.3%; Score 26.6; DB 9; Length 346;
Best Local Similarity 50.4%; Pred. No. 1.6e+02;
Matches 65; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 1629 TTTGTTCAATTCGATTTGTCATTTTATTATCTGTTATCGTCTAAAGTGCTAATTTACC 1688
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OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
RN 1-672
RA Kim N.S., Hahn Y., Oh J.H., Lee J.Y., Ahn H.Y., Chu M.Y., Kim M.R.,
RA Oh K.J., Cheong J.E., Sohn H.Y., Kim J.M., Park H.S., Kim S., Kim Y.S.;
RL "21C Frontier Korean EST Project 2001";
XX Unpublished.
XX UNILIB; 10324; 10324.
XX
XX Contact: Kim YS
CC Genome Research Center
CC Korea Research Institute of Bioscience & Biotechnology
CC 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
CC Tel: +82-42-860-4470
CC Fax: +82-42-860-4409
CC Email: yongsung@mail.kribb.re.kr
CC Plate: 42 row: A column: 05
CC High quality sequence stop: 672.
XX
FH Key Location/Qualifiers
FH
FT source 1..672
FT /db_xref="taxon:9606"
FT /db_xref="UNILIB:10324"
FT /note="Organ: Stomach; Vector: PTZ18RP1; Site 1: EcoRI;
FT Site 2: NotI; The poly (A) + RNA was dephosphorylated with
FT bacterial alkaline phosphatase (BAP) and then decapped with
FT tobacco acid pyrophosphatase (TAP). The decapped intact
FT mRNA was ligated with DNA-RNA linker including EcoR I site
FT by treatment of T4 RNA ligase and the first strand cDNA was
FT synthesized from oligo dt-selected mRNA by priming with
FT dt-tailed vector. The dt-tailed vector was adjusted to have
FT about 60nt. The cDNA vector was circularized with E. coli
FT DNA ligase after digestion of EcoRI which site is also
FT included in vector. An RNA strand converted to a DNA strand
FT by Okayama-Berg method. The obtained cDNA vectors were used
FT for transformation of competent cells E. coli Top10F, by
FT electroporation method. The cDNA libraries constructed by
FT this method are full-length enriched cDNA library."
FT /sex="F"
FT /organism="Homo sapiens"
FT /clone="S21SNU520-42-A05"
FT /clone_lib="S21SNU520"
FT /tissue_type="Stomach"
FT /cell_type="floating aggregates"
FT /cell_line="SNU-520"
FT /lab_host="Top10F"
XX
SQ Sequence 672 BP; 196 A; 134 C; 144 G; 198 T; 0 other;

Query Match 1.3%; Score 26.6; DB 2; Length 672;
Best Local Similarity 56.2%; Pred. No. 1.4e+02;
Matches 50; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1584 TGATAAAATCTCTGAAATACAGGTAATGATTTTGTTCATTCTGAT 1643
| | | | | | | | | | | | | | | | | | | | | |
Db 218 TGGCAAAATGACTTGGTAATTTGTAATGCTGAGTATATTAGTAAAGTTAATTGAT 277
| | | | | | | | | | | | | | | | | | | | | |
QY 1644 TTGTCATTTTATTATCTGTTATCGGTCTA 1672
| | | | | | | | | | | | | | | | | | | | | |
Db 278 GTGTCAACTTTATTTTGTATTTCCTTCCA 306
| | | | | | | | | | | | | | | | | | | | | |

Search completed: March 24, 2003, 01:12:46
Job time : 111 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2003, 00:06:39 ; Search time 1083 Seconds
(without alignments)

9721.340 Million cell updates/sec

Title: US-09-877-633-2

Perfect score: 2028

Sequence: 1 caaaggacaagataataaa.....agtagacagctgtgatgga 2028

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6078533 seqs, 2595712836 residues

Total number of hits satisfying chosen parameters: 12157066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 350 summaries

Database : GenBank-EST

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	648.8	32.0	1014	1	AV079675 AV079675
C 2	644.6	31.8	661	1	AL574115 AL574115
C 3	633.4	31.2	1068	1	AL515908 AL515908
C 4	628.8	31.0	684	2	AW001012 WR91e06.x
C 5	626.6	30.9	932	2	AV726565 AV726565
C 6	601.8	29.7	664	2	BE646471 7e87d05.x
C 7	583.2	28.8	600	2	AW387914 MR4-ST011
C 8	571.0	28.2	669	2	AW387914 MR4-ST011
C 9	551.0	27.2	563	2	AW387761 MR4-ST011
C 10	519.2	25.6	837	2	BE542593 601063983
C 11	519.0	25.6	921	1	AL562740 AL562740
C 12	503.6	24.8	659	2	AW387819 MR4-ST011
C 13	483.6	23.8	551	2	AW387869 MR4-ST011
C 14	483.6	23.8	688	1	AJ449334 AJ449334
C 15	480.6	23.7	499	2	AW387916 MR4-ST011
C 16	466.8	23.0	584	2	AW387858 MR4-ST011
C 17	456.8	22.5	460	1	AA976117 on33b10.s
C 18	450.0	22.2	778	1	AL580786 AL580786
C 19	445.2	22.0	838	1	AL524372 AL524372
C 20	442.4	21.8	614	1	AI536362 ma97f06.y
C 21	423.4	20.9	449	1	AI083909 Qf26b05.x
C 22	418.2	20.6	435	2	AW387755 MR4-ST011
C 23	418.0	20.6	429	2	AV725141 AV725141
C 24	418.0	20.6	429	2	AV729447 AV729447
C 25	418.0	20.6	429	2	AV729585 AV729585
C 26	406.6	20.0	548	2	AV747364 AV747364
C 27	405.8	20.0	1053	1	AL550164 AL550164
C 28	402.2	19.8	977	1	AL514504 AL514504
C 29	401.8	19.8	666	2	BB068522 BB068522
C 30	397.6	19.6	441	2	AW138532 UI-R-B11-

104	216.4	10.7	533	1	AL595594	AL595594	C 177	152	7.5	460	1	AA761443	AA761443	nz26c11.1.b
105	214	10.6	358	1	AA632856	np98a03.s	178	151.6	7.5	713	1	AU0653264	AU0653264	AU0653264
106	212.2	10.5	568	2	AAW77806	ho13d06.x	C 179	151	7.4	586	1	AI889500	AI889500	wto5c11.x
107	211.2	10.4	430	2	BB712477	BB712477	C 180	150.6	7.4	643	2	BB621226	BB621226	BB621226
108	207.8	10.2	477	1	AL120795	DKF2p762E	C 181	150.4	7.4	451	1	AA931505	AA931505	cm90c09.s
109	207.8	10.2	718	1	AL656785	AL656785	C 182	150.2	7.4	259	2	AAW68141	AAW68141	he32h01.x
110	207.6	10.2	504	1	AA874162	vx78f07.r	183	149.4	7.4	527	2	AV667020	AV667020	AV667020
111	207.4	10.2	555	2	AV673706	AV673706	184	148.8	7.3	521	1	AI881896	AI881896	606074G10
112	206.2	10.2	539	1	AI042509	ox62ef12.x	185	147.4	7.3	358	1	AA109888	AA109888	ml98d07.r
113	205.4	10.1	542	2	AA540725	C0136D09.x	186	147.4	7.3	494	2	BE334780	BE334780	u899d05.y
114	205	10.1	604	1	AA218977	zt01c06.s	187	147.2	7.3	390	2	AA413205	AA413205	uq55d12.y
115	204.6	10.1	552	1	AL672935	AL672935	188	147.2	7.3	525	1	AI770419	AI770419	606052D01
116	203.8	10.0	115	2	AAW771091	hm52a05.x	189	147.2	7.3	550	2	BE294166	BE294166	601729J33
117	202.2	10.0	489	1	AL640104	AL640104	190	146.8	7.2	614	2	AAW67876	AAW67876	WS1_1_A04
118	201.6	9.9	288	2	BE478932	163412 BA	191	146.8	7.2	615	2	AAW678614	AAW678614	WS1_1_A04
119	200.6	9.9	354	1	AA590448	vm20d02.r	C 192	145.8	7.2	473	1	AA903164	AA903164	ok53d12.s
120	199.4	9.8	350	1	AA617999	np88d03.s	C 193	145.8	7.2	478	2	AAW649838	AAW649838	xx63a02.x
121	197.4	9.7	549	2	AAW196832	xb13e08.x	C 194	145	7.1	238	2	AAW440104	AAW440104	xx63a02.x
122	194.6	9.6	686	2	AAW071056	AAW071056	195	144.6	7.1	572	1	AJ447416	AJ447416	AJ447416
123	193	9.5	371	1	AA546195	vk05b09.r	C 196	143.6	7.1	443	1	AA642451	AA642451	rs30c02.s
124	190	9.4	583	2	AAW67124	da63c02.y	197	143.6	7.1	554	1	AL639060	AL639060	AL639060
125	187.8	9.3	610	2	BE299569	600944483	198	143.4	7.1	592	2	BE439891	BE439891	HTM1_486F
126	186.2	9.2	442	2	AAW377517	QVO-CT022	199	142.8	7.0	451	2	BB783001	BB783001	BB783001
127	185.2	9.1	518	1	AA825580	cd57f01.s	200	142.6	7.0	639	1	AA161279	AA161279	z055h04.r
128	184.2	9.1	595	2	AAW15372	f135c09.y	C 201	142	7.0	546	1	AJ447705	AJ447705	AJ447705
129	183.6	9.1	640	2	BB624364	BB624364	C 202	141	7.0	462	2	AAW122856	AAW122856	UI-N-BH2
130	182.4	9.0	184	1	AA911425	oe71b06.s	203	140.8	6.9	598	2	AAV26907	AAV26907	AV926907
131	180.6	8.9	510	1	AI281993	qm21d11.x	204	140.8	6.9	632	2	AAV913199	AAV913199	AAV913199
132	179.2	8.8	391	1	AA083725	zm62f02.r	205	140.8	6.9	653	2	AAV926906	AAV926906	AAV926906
133	179.2	8.8	717	2	BB618308	601462688	206	140.6	6.9	413	2	BE272845	BE272845	601171085
134	179	8.8	544	1	AI828791	tw70807.x	C 207	140	6.9	512	1	AA230338	AA230338	mw04c12.r
135	177	8.7	652	1	AJ451936	AJ451936	C 208	139	6.9	399	1	AA112736	AA112736	zn46d11.r
136	176.6	8.7	649	1	AJ453343	AJ453343	C 209	139	6.9	644	1	AL514503	AL514503	AL514503
137	175.8	8.7	545	1	AL633246	AL633246	210	138.6	6.8	464	2	BB782048	BB782048	BB782048
138	175.6	8.7	625	1	AJ454239	AJ454239	211	138.2	6.8	458	2	AAW564408	AAW564408	LG1_292.D
139	175.4	8.6	667	2	BB655891	BB655891	212	138.2	6.8	620	1	AL786446	AL786446	AL786446
140	172.4	8.5	556	1	AL632992	AL632992	C 213	137.8	6.8	478	1	AA415300	AA415300	vc99g02.s
141	172	8.5	661	1	AL639281	AL639281	C 214	137.4	6.8	451	2	AAW831229	AAW831229	UI-N-BH2
142	171.4	8.5	767	1	AL584137	AL584137	215	136.4	6.7	591	2	AAW831229	AAW831229	rm12g02.y
143	169.6	8.4	241	1	AA591374	v166a11.r	216	136.2	6.7	565	1	AL830019	AL830019	AL830019
144	168.2	8.3	626	1	AI036359	ub56a07.r	217	135.6	6.7	826	2	AAW48309	AAW48309	BRY_1838
145	167.4	8.3	375	1	AI414398	ma97f06.x	218	135.2	6.7	729	2	BE413842	BE413842	SCU0003.F0
146	167.4	8.3	582	2	BE409480	601303887	219	134.6	6.6	631	2	AAV926670	AAV926670	AV926670
147	167	8.2	181	1	AA301454	EST14395	C 220	134.6	6.6	634	2	AAV941294	AAV941294	AAV941294
148	166.2	8.2	719	1	AJ446154	AJ446154	C 221	134.4	6.6	441	2	AAW524124	AAW524124	UI-R-BOO-
149	166	8.2	501	1	AA656943	v-25c02.r	222	134.2	6.6	398	2	AAV926671	AAV926671	AAV926671
150	166	8.2	708	1	AJ455143	AJ455143	223	134.2	6.6	633	2	BE510705	BE510705	946054H08
151	165.6	8.2	464	1	AA808521	oe55e09.s	224	134.2	6.6	752	2	BE407968	BE407968	601299345
152	165.4	8.2	601	1	AL602414	DKF2p686H	225	134	6.6	585	2	AAW684123	AAW684123	NF012F07N
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154	163.8	8.1	396	2	AAW023913	dfe1f09.y	C 227	133.6	6.6	565	2	BB638678	BB638678	946012E11
155	163.6	8.1	644	2	BB625420	BB625420	C 228	132.8	6.5	423	1	AAJ223209	AAJ223209	zr06c11.s
156	163.2	8.0	533	2	BE509875	946068A10	229	132.8	6.5	524	2	BE363855	BE363855	FI1_10.B0
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158	162.2	8.0	480	2	BB680896	BB680896	C 231	132.6	6.5	687	1	AL647152	AL647152	AL647152
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160	161.6	8.0	2408	3	AAV103907	zeta may8	C 233	131.8	6.5	701	1	AU056313	AU056313	AAU056313
161	161.2	7.9	367	1	AA304362	EST17171	234	131.4	6.5	314	1	AI006388	AI006388	ua71d10.r
162	159.4	7.9	468	1	AI351512	qf06b007.x	C 235	131.4	6.5	426	1	AA128950	AA128950	zo10f10.s
163	158.2	7.8	683	2	AAV913489	AAV913489	236	131	6.4	663	2	AAW684792	AAW684792	NF021B07N
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165	157.4	7.8	612	1	AL594068	AL594068	C 238	130.8	6.4	663	1	AL650683	AL650683	AL650683
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172	155.4	7.7	796	2	AAW48525	BBY_947.B	245	128.6	6.3	263	2	BE084264	BE084264	PM3-BT065
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253	125.8	6.2	367	2	BE590994	WHL1655-1	BE590994	108.2	5.3	286	1	AA120589	AA120589	mn10b02.Y
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255	125.2	6.2	492	1	AT189909	SB96a05.Y	AT189909	108	5.3	687	1	AL505513	AL505513	AL505513
256	124.8	6.2	460	1	AA080251	mm34a10.Y	AA080251	107.8	5.3	179	1	AA867580	AA867580	vy02c09.Y
257	124.6	6.1	643	2	BB626730	BB626730	BB626730	107.6	5.3	611	2	AV566554	AV566554	AV566554
258	124.4	6.1	463	2	AW759875	sl55c03.Y	AW759875	107.2	5.3	421	2	AV925106	AV925106	AV925106
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260	123.8	6.1	652	1	AL631270	AL631270	AL631270	106.6	5.3	277	2	AV349038	AV349038	AL792789
261	123.4	6.1	467	2	AW162791	au87b11.Y	AW162791	106.2	5.2	555	1	AL792789	AL792789	AL792789
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263	122.4	6.0	422	2	AV411756	AV411756	AV411756	106	5.2	541	1	AL935311	AL935311	wp16905.X
264	122.4	6.0	481	1	AL383348	MCBC13E12	AL383348	106	5.2	594	2	AW443003	AW443003	AV553924
265	122	6.0	396	2	AW208258	M10914e	AW208258	105.6	5.2	526	2	AV553924	AV553924	AV553924
266	122	6.0	538	2	AV914848	AV914848	AV914848	105	5.2	277	2	BB231288	BB231288	BB231288
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270	120.8	6.0	177	2	AW388025	MR4-ST011	AW388025	104.8	5.2	691	2	BE280656	BE280656	601155912
271	120.8	6.0	698	2	AW688577	NRFO09B11S	AW688577	104.2	5.1	184	2	BE226560	BE226560	ia22g01.Y
272	120.4	5.9	404	2	BB688632	BB688632	BB688632	104.2	5.1	328	2	AW230231	AW230231	up28e08.Y
273	120	5.9	410	1	AL920785	wn82a05.X	AL920785	103.4	5.1	479	2	BB858104	BB858104	BB858104
274	119.6	5.9	401	2	BE519228	946094G04	BE519228	103	5.1	1136	3	AY105053	AY105053	Zea mays
275	119.4	5.9	790	2	BE410845	601301148	BE410845	102.8	5.1	282	2	BB231050	BB231050	BB231050
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278	118.8	5.9	436	2	BE608893	sn97e02.Y	BE608893	102.2	5.0					
279	118	5.8	521	1	AL640119	ms73b12.Y	AL640119	102.2	5.0					
280	118	5.8	556	2	BE344805	946029B04	BE344805	102.2	5.0					
281	117.8	5.8	322	2	BE681140	d906d04.Y	BE681140	102.2	5.0					
282	117.4	5.8	500	2	BB702955	BB702955	BB702955	102.2	5.0					
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284	116.8	5.8	314	2	BE298153	BB298153	BE298153	102.2	5.0					
285	116.8	5.8	411	2	BE100355	UI-R-BJ1	BE100355	102.2	5.0					
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287	116.8	5.8	489	2	BE450350	EST401237	BE450350	102.2	5.0					
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309	111.8	5.5	591	2	AV932104	AV932104	AV932104	102.2	5.0					
310	111.4	5.5	855	2	BE053277	GA_Ea003	BE053277	102.2	5.0					
311	111.2	5.5	425	2	BE656604	UI-N-BH0	BE656604	102.2	5.0					
312	111	5.5	380	2	BE606816	WHE0906.E	BE606816	102.2	5.0					
313	111	5.5	432	1	AA405604	zw39c08.Y	AA405604	102.2	5.0					
314	110.2	5.4	380	2	BE428872	MTD011.G0	BE428872	102.2	5.0					
315	110	5.4	453	2	BB859739	BB859739	BB859739	102.2	5.0					
316	109.8	5.4	395	1	AI282952	qt82g08.X	AI282952	102.2	5.0					
317	109.6	5.4	456	2	BB861965	BB861965	BB861965	102.2	5.0					
318	109.6	5.4	502	2	AW508690	sl35c03.Y	AW508690	102.2	5.0					
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320	109.2	5.4	321	2	BE438826	BCD98.WHE	BE438826	102.2	5.0					
321	109	5.4	409	1	AA716278	zg91b04.S	AA716278	102.2	5.0					
322	108.8	5.4	544	2	BE600935	PI1_95_A0	BE600935	102.2	5.0					

ALIGNMENTS

RESULT 1
 AV079675 1014 bp mRNA linear EST 24-OCT-2001
 LOCUS AV079675 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
 DEFINITION clone 2210410K23, mRNA sequence.
 ACCESSION AV079675
 VERSION AV079675.2 GI:16381140
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1014)
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hata, A.,
 Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda,
 M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki,
 Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki,
 D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
 Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
 Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 TITLE RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 JOURNAL Unpublished (2001)
 COMMENT On Jun 25, 1999 this sequence version replaced gi:5211123.
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 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayashizaki, Y., Sugahara, Y., Shibata, K., Itoh,
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 prepare full-length cDNA libraries for rapid discovery of new
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Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences *Mamm. Genome* 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopaedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

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RESULT 2
AL574115/c
LOCUS
DEFINITION AL574115 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI040YK06 3
661 bp mRNA linear EST 16-FEB-2001
prime, mRNA sequence.
ACCESSION AL574115
VERSION AL574115.1 GI:12934008
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 661)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/tissue_types="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA

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was primed with a NotI-oligo(dT) primer. Five prime end
cloned, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT	119 a	179 c	178 g	181 t	4 others
ORIGIN					
Query Match	31.8%; Score 644.6; DB 1; Length 661;				
Best Local Similarity	99.1%; Pred. No. 1.9e-153;				
Matches 655; Conservative	2; Mismatches 3; Indels 1; Gaps 1;				
Qy	527	CTGGCAGCATAGCACTCTCTGGAAAGTCCAGAGCTTAATCTGCCCCCAGCGTGAAT	586		
Db	661	CTGGCAGCATAGCAATCTCTGGAAAGTCCAGAGCTTAATCTGCCCCCAGCGTGAAT	602		
Qy	587	CCACCCCGTCTTGA AAAACTGAAGGCTGCTCACAGCTACAAACCCGAAAGAGTTTGAGT	646		
Db	601	CCACCCCGTCTTGA AAAACTGAAGGCTGCTCACAGCTACAAACCCGAAAGAGTTTGAGT	542		
Qy	647	GGAAATCTGAAAAGCGGCGGTGTTCATCATCAAGAGTACTCTGAGGACGACATCCACC	706		
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Db	481	GCTCCATTAAAGTACTCCATCTGTGTAGCAGACGCGCAACGCGCTGGACAGCG	422		
Qy	767	CTTTCGCTGCATGAGCAGCAAGGGGCCGTCTACCTGCTTTCAGCGTCAATGGGAGTG	826		
Db	421	CTTTCGCTGCATGAGCAGCAAGGGGCCGTCTACCTGCTCTNCAAGCGTCAATGGGAGTG	362		
Qy	827	GGCAATTTTGTGGGTGGCGGAGATGAAGTCCCGCTGGACTACGGCACGAGTCCCGGG	886		
Db	361	GGCAATTTTGTGGGTGGCGGAGATGAAGTCCCGCTGGACTACGGCACGAGTCCCGGG	302		
Qy	887	CTGTGCTCTCAGGACAACTGGAAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGATG	946		
Db	301	CTGTGCTCTCAGACNAGTGGNAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGATG	242		
Qy	947	TACCCCAATAACAGCTCCGGGCATCAGGCTGGAGAATAACGACAAACAAACCGGTCAAA	1006		
Db	241	TACCCCAATAACAGCTCCGGGCATCAGGCTGGAGAATAACGACAAACAAACCGGTCAAA	182		
Qy	1007	ACTCCCGGACACCCAGGAGTGCCTTTAGAAAAGCCAGCAAGTGTGAAAATTATCA	1066		
Db	181	ACTCCCGGACACCCAGGAGTGCCTTTAGAAAAGCCAGCAAGTGTGAAAATTATCA	122		
Qy	1067	GTTCTCTACAGCACACACCTCCATCTTCGACACTTGTCTACTACGAGAGCGCCA-G	1125		
Db	121	GTTCTCTACAGCACACACCTCCATCTTCGACACTTGTCTACTACGAGAGCGCCAGG	62		
Qy	1126	AGGAGGAGGAGTGGTGGCGAAGGCGGAGTTCGAAAACAAACATAGCGGGCGAACCA	1185		
Db	61	AGGAGGAGGAGTGGTGGCGAAGGCGGAGTTCGAAAACAAACATAGCGGGCGAACCA	2		
Qy	1186	G 1186			
Db	1	G 1			
RESULT 3					
AL515908/c					
LOCUS					
DEFINITION	AL515908 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA001YB18 3				
ACCESSION	prime, mRNA sequence.				
VERSION	AL515908				
KEYWORDS	EST.				

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1068)
TITLE	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL	Full-length cDNA libraries and normalization
COMMENT	Unpublished (2001)
FEATURES	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
source	Location/Qualifiers
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	/sex="male"
	/tissue_type="neuroblastoma cells"
	/lab_host="DH10B"
	/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT	382 a 217 c 187 g 275 t 7 others
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Query Match	31.2%; Score 633.4; DB 1; Length 1068;
Best Local Similarity	98.0%; Pred. No. 1.5e-150;
Matches 646; Conservative	5; Mismatches 6; Indels 2; Gaps 1;
QY	1370 CACTAATAAAGGAGTATTTTGTGCTGAGCTTATCAATCAGACTGATCTAATGTGAAT 1429
Db	1068 CACTAATAAAGGTA--TTTGTGCTGAGCTTATCAATCAGACTGATCTAATGTGAAT 1011
QY	1430 GTAAGTATCTTTAAAAACAAAGCATCTATTTGGCAGAAATTTGTCTTAAATCAGTC 1489
Db	1010 GTGAGTATCTTAAAAACAAAGCATCTTTTGGCAGAAATTTGTCTTAAATCAGTC 951
QY	1490 ATTGATATCTGTGAGACTTCATATTTCTCATCCCTTTATTTGCTTTTAGCAACATAA 1549
Db	950 ATTGATATCTGTGAGACTTCATATTTCTCATCCCTTTATTTGCTTTTAGCAACATAA 891
QY	1550 GAAACCATGAGTCATTTGCTGATTTAGAGTATTTCTGATAAATCTCTTGAATACTGAA 1609
Db	890 GAAACCATGAGTCATTTGCTGATTTAGAGTATTTCTGATAAATCTCTTGAATACTGAA 831
QY	1610 ATCAAAAGGTTAATGATTTTGTTCATTCTGATTTGTCAATTTATTTATCTGTATCGGT 1669
Db	830 ATCAAAAGGTTAATGATTTTGTTCATTCTGATTTGTCAATTTATTTATCTGTATCGGT 771
QY	1670 CTAAAGTGTAAATTTACCCATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAA 1729
Db	770 CTAAAGTGTAAATTTACCCATTTGATTTTCTGCTAACAACAGATAAATTTTAAATTTTCAA 711
QY	1730 ATTTGGCAGACACTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1789
Db	710 ATTTGGCAGACACTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 651
QY	1790 GAACAGCCACCGCTCCCTCAGCTGTCTGTGTGTCGATTTGGGCTGGATGTTTGGGGCAT 1849
Db	650 GAACAGCCACCGCTCCCTCAGCTGTCTGTGTGTCGATTTGGGCTGGATGTTTGGGGCAT 591
QY	1850 GATGTGTGAGGAACATGGAAGGTGCTTTAGGTCTGTTTCTGAGGTCTGGGCATCTTTTGTGTTG 1909

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Db 590 GATGTGTGGAGGAACACTCGAAGGTGCTTTAGGTCGTGGTTCAGGGTCGGGCATTTCTTTGTTG 531
QY 1910 TTTGACACATCTTTTAAATTTTACACCTTTTCTTAAAGAAATCTTAATGCCGCTCTTAAGTTT 1969
Db 530 TTTGACACATCTTTTAAATTTTACACCTTTTCTTAAAGAAATCTTAATGCCGCTCTTAAGTTT 471
QY 1970 TTATACCAATAAGTCTGAGCTTTAAAGTGTAGGATCTGGTAGACAGACAGTGTGATGGA 2028
Db 470 TTATACCAATAAGTCTGAGCTTTAAAGTGTAGGATCTGGTAGACAGACAGTGTGATGGA 412

RESULT 4
AW001012/c
LOCUS          684 bp      mRNA      linear      EST 08-MAR-2000
DEFINITION     wr91e06.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2495074 3'
                similar to TR:064526 O64526 YUP812R.13 PROTEIN. ;, mRNA sequence.
ACCESSION      AW001012
VERSION        AW001012.1 GI:5847928
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 684)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
JOURNAL         Unpublished (1997)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cgapsb@lemail.nih.gov
                Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                Emmert-Buck, M.D., Ph.D.
                cDNA Library Preparation: M. Bento Soares, Ph.D.
                DNA Sequencing by: Washington University Genome Sequencing Center
                Clone distribution: NCI-CGAP clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                www.bio.llnl.gov/bbrp/image/image.html
                Insert Length: 1194 Std Error: 0.00
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                High quality sequence stop: 476.
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                /clone_lib="NCI_CGAP_Kid11"
                /lab_host="DH10B"
                /notes="Organ: kidney; Vector: pTT73D-Pac (Pharmacia) with
                a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
                Plasmid DNA from the normalized library NCI CGAP Kid1 was
                prepared, and as circles were made in vitro. Following HAP
                purification, this DNA was used as tracer in a subtractive
                hybridization reaction. The driver was PCR-amplified cDNAs
                from a pool of 5,000 clones made from the same library
                (clones IDs 1322376-13223911, 1456007-1456775, and
                1500552-1502855). Subtraction by Bento Soares and M.
                Fatima Bonaldo."
BASE COUNT     175 a 178 c 160 g 171 t
ORIGIN
Query Match    31.0%; Score 628.8; DB 2; Length 684;
Best Local Similarity 97.8%; Pred. No. 2e-149;
Matches 669; Conservative 0; Mismatches 12; Indels 3; Gaps 3;

QY 725 TCTGGTGTAGCAGACAGCGAACAGCGCTGGACAGCGCTTCGGCTGCATGACGA 784
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QY 785 GCAAGGGCCCGTCTACCTCTTACGCTCAATGGAGTGGGCATTTTGTGGGGTGG 844
Db 623 GCAAGGGCCCGTCTACCTCTTACGCTCAATGGAGTGGGCATTTTGTGGGGTGG 564

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QY 845 CCAGATGAAGTCCCCCGTGGACTACGGCACCAAGTGCCTGGGGTCTGGTCTCAGGACAAGT 904
Db 563 CCAGATCAAGTCCCCCGTGGACTATGGCACCAAGTGCCTGGGGTCTGGTCTCAGGACAAGT 504
QY 905 GGAAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGGATGTACCAATTAACAGGTCC 964
Db 503 GGAAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGGATGTACCAATTAACAGGTCC 444
QY 965 GGACATCAGGCTGGAGAAATTAACGACAAACCGGTACAAAACCTCCCGGGACACACCCAGG 1024
Db 443 GGACATCAGGCTGGAGAAATTAACGACAAACCGGTACAAAACCTCCCGGGACACACCCAGG 384
QY 1025 AGTGCCCTTTAGAAAAGCCAGCAAGTGTCTGAAAATTTATCAGTTCTTACAAGCACACAA 1084
Db 383 AGTGCCCTTTAGAAAAGCCAGCAAGTGTCTGAAAATTTATCAGTTCTTACAAGCACACAA 324
QY 1085 CTTCCATC-TTCCAGCAGCTTTGCTCACTACGAGAGAGGCCA-CAGGAGGAGGAGGTGGT 1142
Db 323 CTTCCATC-TTGGACGACTTTTGTCTACTACGAGAGAGGCCA-CAGGAGGAGGAGGTGGT 264
QY 1143 CGCAAGGAACGGCAGAGTTCGAAAACAAATGAGGGGGAACCAAGTTTCTTTACATGTTCTA 1202
Db 263 CGCAAGGAACGGCAGAGTTCGAAAACAAATGAGGGGGAACCAAGTTTCTTTACATGTTCTA 204
QY 1203 ACCTTTGACTTTGAAAACAGCTTTTAAACACAGTGTGTTGTCAGTCCAGTGTGTGCTCC 1262
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QY 1323 TCTGCACTTTATTTGTTACTTTTCTATGTTATTAATCCTCTAGAAGTCACTAATAAGGA 1382
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QY 1383 GTATTTTCTTCTCAGCTTATCA 1406
Db 23 GTA-TTTTCTTCTCAGCTTATCA 1

RESULT 5
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LOCUS          932 bp      mRNA      linear      EST 17-OCT-2000
DEFINITION     AV726565 HTC Homo sapiens cDNA clone HTCAE08 5', mRNA sequence.
ACCESSION      AV726565
VERSION        AV726565.1 GI:10835986
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 932)
AUTHORS        Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
                Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, B., Xu
                S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
                Chen, J., Chen, Z. and Han, Z.
TITLE          Homo sapiens cDNA HTC clones
JOURNAL        Unpublished (2000)
COMMENT        Contact: Zeguang Han
                Chinese National Human Genome Center at Shanghai
                351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
                201203, P. R. China
                Tel: 86-21-50801919 (ex.45)
                Fax: 86-21-50801922
                Email: hanzg@hgc.sh.cn
                This clone is available at CHGC in Shanghai.
FEATURES       Location/Qualifiers
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QY 1280 TTGCATCTTTGCCCTTCTTGTGCTGTTGATTTTGGCCAGATGGATCTGCATTTATTTGTAC 1339
Db 124 TTGCATCTTTGCCCTTCTTGTGCTGTTGATTTTGGCCAGATGGATCTGCATTTATTTGTAC 65
QY 1340 TTTTCTATGTATTATATCTCTAGAGAGTCACTAATAAAGGAGTATTTTTTTT 1393
Db 64 TTTTCTATGTATTATATCTCTAGAGAGTCACTAATAAAGGAGTATTTTTTTT 11

RESULT 7
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LOCUS AW387914 600 bp mRNA linear EST 04-FEB-2000
DEFINITION MR4-ST0119-071099-010-F01 ST0119 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW387914
VERSION AW387914.1 GI:6892573
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 600)
REFERENCE HCGP http://www.ludwig.org.br/ORESTES.
AUTHORS The FAPESP/LICR Human Cancer Genome Project
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-ST0119-071099-010-F01&t3=1999-10-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 581.
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/clone_lib="ST0119"
/dev_stage="Adult"
/notes="Organ: stomach; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 124 a 169 c 151 g 156 t
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Query Match 28.8%; Score 583.2; DB 2; Length 600;
Best Local Similarity 99.3%; Pred. No. 7.8e-138;
Matches 596; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 676 ATCAAGAGTACTCTGAGGACGACATCCACCGCTCCATTAGTACTCCATCTGGTGATGC 735
Db 600 ATCAAGAGTACTCTGAGGACGACATCCACCGCTCCATTAGTACTCCATCTGGTGATGC 541
QY 736 ACAGAGCAGCGACACAGCGCTGGACAGCGCTTCGCTGCATGACGAGGAGGCC 795
Db 540 ACAGAGCAGCGACATCAAGCGCTGGACAGCGCTTCGCTGCATGACGAGGAGGCC 481
QY 796 GTCTACCTGCTCTTACGGTCAATGGGAGTGGGCAATTTTGTGGGTGGCCGAGATCAAG 855
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QY 856 TCCCCCGTGGACTACGGCACAGTGCCTGGGGTCTGGTCTCAGGACAAAGTGGAAGGGGAAG 915
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Db 360 TTTGATCTCCAGTGGATTTTGTAAAGATGTACCCCAATACCAAGCTCCCGCACATCAGG 301
QY 976 CTGAGAGATTAACGACAAACAAACCGGTCAAAAACCTCCCGGACACCCAGGAGGTGCCCTTA 1035
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QY 1155 CAGAGTCGAAACAAACAAATGAGGCGCAACAGATTTCTTACATGTTCTAAAGTTTGACTTT 1214
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DEFINITION MAGE resequencences, MAGH Homo sapiens cDNA, mRNA sequence.
ACCESSION AW964022
VERSION AW964022.1 GI:8153858
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 669)
REFERENCE Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt,
AUTHORS I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 196
Seq primer: Reverse.
FEATURES
Location/Qualifiers
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Query Match 28.2%; Score 571; DB 2; Length 669;
Best Local Similarity 97.4%; Pred. No. 1e-134;
Matches 591; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 1396 TCAGCTTATCAATCAGACTGATCTAATGTGAATGTAAAGTATCCTTAAAAACAAAGCATC 1455
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QY 1576 GAGTATTTCTGATAAAATCTCTTGAATAATCTGAAATCAAAAGGTTAAATGATTTTGTTC 1635
 Db GAGTATTTCTGATAAAATCTCTTGAATAATCTGAAATCAAAAGGTTAAATGATTTTGTTC 240

QY 1636 ATTCGATTTGTCATTTTATTTATCTGTTATCGTCTAAAGTCTTAATTTACCATTGAT 1695
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QY 1696 TTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTTGGCAGACAC-TTTTTTTTTTTTT 1754
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QY 1755 TTGAAATCTTTTCTTCCAGATCTGTTGCCACTGAACAGCCACCCGTCCTCACTGTC 1814
 Db TTGAAATCTTTTCTTCCAGATCTGTTGCCACTGAACAGCCACCCGTCCTCACTGTC 420

QY 1815 CTGGTCTCCGATTTGGCTGGATGTTGGGCGCATGATGTGGAGGAACCTGGAAGGTGC 1874
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QY 1875 TTTAGTCTGTTTCAAGGTCGGGCTCTTTGTTGTTTGCACATCTTTTAAATTTTACA 1934
 Db TTTAGTCTGTTTCAAGGTCGGGCTCTTTGTTGTTTGCACATCTTTTAAATTTTACA 540

QY 1935 CTTTTTCTTAAAGATTTCTAATGCGCTTAAAGTTTATACCAATAATCTGAGCTTTTAA 1994
 Db CTTTTTCTTAAAGATTTCTAATGCGCTTAAAGTTTATACCAATAATCTGAGCTTTTAA 600

QY 1995 GTGTAGG 2001
 Db ATGGTGG 607

RESULT 9
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 LOCUS MR4-ST0118-041099-010-C01 ST0118 Homo sapiens cDNA, mRNA linear EST 04-FEB-2000
 DEFINITION MR4-ST0118-041099-010-C01 ST0118 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW387761
 VERSION AW387761.1 GI:6892420
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 563)
 HCGP <http://www.ludwig.org.br/ORESTES>.
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC0&t2=MR4-ST0118-041099-010-C01&t3=1999-10-04&t4=1>)
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FEATURES

source

/db_xref="taxon:9606"
 /clone_lib="ST0118"
 /note="Organ: stomach; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No.196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 116 a 161 c 139 g 147 t

ORIGIN

Query Match 27.2%; Score 551; DB 2; Length 563;

Best Local Similarity 99.8%; Pred. No. 1.2e-129;

Matches 562; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 713 TTAAGTACTCCATCTGTGTAGCAGAGCAGCGCAACAGCGCTTGACAGCGCTTCC 772

Db 563 TTAAGTACTCCATCTGTGTAGCAGAGCAGCGCAACAGCGCTTGACAGCGCTTCC 504

QY 773 GCTGATGAGCAGCAAGGGGCGCTTACCTGCTCTTCAAGCGTCAATGGAGTGGGCAAT 832

Db 503 GCTGATGAGCAGCAAGGGGCGCTTACCTGCTCTTCAAGCGTCAATGGAGTGGGCAAT 444

QY 833 TTTTGGGTGGCCGAGATGAAGTCCCGCTGGACTACGGCACAGTGCCTGGGTCTGGT 892

Db 443 TTTTGGGTGGCCGAGATGAAGTCCCGCTGGACTACGGCACAGTGCCTGGGTCTGGT 384

QY 893 CTCAGCAAGTGGGAAGGGAAGTTTGTATGCTCAGTGGATTTTCTTAAGGATGTACCA 952

Db 383 CTCAGCAAGTGGGAAGGGAAGTTTGTATGCTCAGTGGATTTTCTTAAGGATGTACCA 324

QY 953 ATAACAGCTCCGGCACATCAGGCTGGAGAAATACGACAAACCGGTCAAAAATCCC 1012

Db 333 ATAACAGCTCCGGCACATCAGGCTGGAGAAATACGACAAACCGGTCAAAAATCCC 264

QY 1013 GGGACACCCAGAGTGCCTTTAGAAAAAGCAACAGTGTGAAAAATTATCAGTTCT 1072

Db 263 GGGACACCCAGAGTGCCTTTAGAAAAAGCAACAGTGTGAAAAATTATCAGTTCT 204

QY 1073 ACAAGCACACACCTCCATCTTCGAGCACTTTGCTACCTACGAGAGCGCA-GAGGAGG 1131

Db 203 ACAAGCACACACCTCCATCTTCGAGCACTTTGCTACCTACGAGAGCGCGCAGGAGGAGG 144

QY 1132 AGGAGTGTGTGGCAAGAAACGGCAGAGTCGAAACAAACATGAGGGCGAAACAGTTTCT 1191

Db 143 AGGAGTGTGTGGCAAGAAACGGCAGAGTCGAAACAAACATGAGGGCGAAACAGTTTCT 84

QY 1192 TACATGTTTCTAACGTTTGAATTTGAAAAACAGTTTAAAAACAGTGTCTGTGGTCACTCCA 1251

Db 83 TACATGTTTCTAACGTTTGAATTTGAAAAACAGTTTAAAAACAGTGTCTGTGGTCACTCCA 24

QY 1252 GTGTGTCGTCCTCGTGGGGGTT 1274

Db 23 GTGTGTCGTCCTCGTGGGGGTT 1

RESULT 10

BE542593 837 bp mRNA linear EST 09-AUG-2000

LOCUS 601063983F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450261 5',

DEFINITION mRNA sequence.

ACCESSION BE542593

VERSION BE542593.1 GI:9771238

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 837)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)


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QY 1804 CCTCACTCTCTGCTGTCCTGATTTGGGCTGGATGGTGTGGGGCATGATGTGGAGGAA 1863
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Db 621 CCTCACTCTCTGCTGTCCTGATTTGGGCTGGATGGTGTGGGGCATGATGTGGAGGAA 562
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QY 1864 CTGGAGGTCCTTTAGGTCCTGGTCAGGTCGGGCATCTCTTTGTTGGTTCACATCTTTT 1923
|||||
Db 561 CTGGAAGGBCCTTTAGTCTGGTTCAGGTCGGGCATCTCTTTGTTGGTTCACATCTTTT 502
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QY 1924 TAAATTTTACACCTTTCTTAAGAATTTCTAATGCCGCTTTAAGTTTATATACCAATAATG 1983
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Db 501 TAAATTTTACACCTTTCTTAAGAATTTCTAATGCCGCTTTAAGTKTTATACCAATAATG 442
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QY 1984 CTGAGCTTTAAGTGTAGGATCTGGTAGTACAGACAGTGTGATGGA 2028
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Db 441 CTGAGCTTTAAGTGTAGGATCTGGTAGGACAGACAGTGTGATGGA 397
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RESULT 12
AW387819 AW387819 659 bp mRNA linear EST 04-FEB-2000
LOCUS MR4-ST0118-021299-021-a06 ST0118 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW387819
ACCESSION AW387819
VERSION AW387819.1 GI:6892478
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 659)
HGCP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR4&t2=MR4-ST0118-
021299-021-a06&t3=1999-12-02&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 658.
Location/Qualifiers
1..659
/organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 178 a 175 c 179 g 127 t
ORIGIN

Query Match 24.8%; Score 503.6; DB 2; Length 659;
Best Local Similarity 95.8%; Pred. No. 1.5e-117;
Matches 571; Conservative 0; Mismatches 19; Indels 6; Gaps 5;

QY 559 CAGCCTAATTTCTGCCCGCAGGTCGAATCCACCCCGTCTCTGAAACCTGAAGGCTGCT 618
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Db 22 CAGCCTAATTTCTG--CCAGCGTCGAATCCACCCCGTCTCTGAAACTGAAGGCTGCTC 79
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QY 619 CACAGCTTACACCCGAAAGATTTGAGTGAATCTTGAAA-GCGGGCGTGTTCATCAT 677
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Db 80 AGGACTACAAACCGAAGAGTTTGAATGGAACTCTGAAAAGCGGGCGTGTGTTTCATCAT 139
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QY 678 CAA-GAGCTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCCATCTGGTGTAGCA 736
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Db 140 CAATGAGCTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCCATCTGGTGTAGCA 199
|||||
QY 737 CAGACACGGCAACAAAGCGCTTGGACAGCGCTTCCGCTGTCATGAGCAGCAGAGGGGCGG 796
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Db 200 CAGACACGGCAACAAAGCGCTTGGACAGCGCTTCCGCTGTCATGAGCAGCAGAGGGGCGG 259
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QY 797 TCTACTCTCTTCTTCAAGCTCAATGGAGTGGGCATTTTGTGGGTGGCCGAGAGTGAAGT 856
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Db 260 TCTACTCTCTTCTTCAAGCTCAATGGAGTGGGCATTTTGTGGGTGGCCGAGAGTGAAGT 319
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QY 857 CCCCCGTGGACTACGGCACCAAGTGGC--GGGGTCTGGTCTCAGGACAAAGTGGAGGGGAAG 915
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Db 320 CCCCCGTGGACTACGGCACCAAGTGGC--GGGGTCTCAGGACAAAGTGGAGGGGAAG 379
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QY 916 TTTGATGTCCAGTGGATTTTGTAAAGATGTACCC--ATAACACAGCTCCGCGCATCAG 974
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Db 380 TTTGATGTCCAGTGGATTTTGTAAAGATGTACCCAAATAACACAGCTCCGCGCATCAG 439
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QY 975 GCTGGAGAATAACGACACAAACCGGTCAAACTCCCGGGACACCCAGGAGGTGCCCTT 1034
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Db 440 GCTGGAGAATAACGACACAAACCGGTCAAACTCCCGGGACACCCAGGAGGTGCCCTT 499
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QY 1035 AGAAAAAGCCAAAGCAAGTGTCTGAAAATTTATCAAGTCTCTACAAAGCACACACCTCCATCTT 1094
|||||
Db 500 AGAAAAAGCCAAAGCAAGTGTCTGAAAATTTATCAAGTCTCTACAAAGCACACACCTCCATCTT 559
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QY 1095 CGACGACTTTGTCTACTACGAGAGCGCCAGAGGAGGAGGAGGTGGTGGCGAAGGA 1150
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RESULT 13
AW387869/c AW387869 551 bp mRNA linear EST 04-FEB-2000
LOCUS MR4-ST0118-151299-023-d10 ST0118 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW387869
ACCESSION AW387869
VERSION AW387869.1 GI:6892528
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 551)
HGCP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR4&t2=MR4-ST0118-
151299-023-d10&t3=1999-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 484.
Location/Qualifiers
1..551
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0118"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products

FEATURES
source
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derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 111 a 155 c 143 g 142 t
ORIGIN
Query Match 23.8%; Score 483.6; DB 2; Length 551;
Best Local Similarity 96.8%; Pred. No. 1.7e-112;
Matches 536; Conservative 0; Mismatches 14; Indels 4; Gaps 4;

QY 716 AGTACTCCATCTGGTGTAGACACAGACGCGCAACAGCGCCTGGACAGCGCCTTCGGCT 775
DB 551 AGTACTCCATCTGGT-TAGCACAGAGACGCGCAACAGCGCCTGG-CAGCGCCTTCGGCT 494
QY 776 GCATGACACAGAGGGCCGCTTACCTGCTTTCACGGCTCAATGGGAGTGGGCAATTTT 835
DB 493 GCATGACACAGAGGGCCGCTTACCTGCTTTCACGGCTCAATGGGAGTGGGCAATTTT 434
QY 836 GTGGGGTGGCGGAGATGAAGTCCCGCTGGACTACGGCACAGTGGCGGGGTCTGGTCTC 895
DB 433 CTGGGGTGGCGGAGATGAAG-CCCGCTGGACTACGGCACAGTGGCGGGGTCTGGTCTC 375
QY 896 AGGACAAGTGGAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGGATGTACCCAAATA 955
DB 374 AGGACAAGTGGAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGGATGTACCCCAATA 315
QY 956 ACCAGCTCCCGGCACATCAGCTGGAGATTAACGACACAAACCGGTCACAAACTCCCGGG 1015
DB 314 ACCAGCTCCCGGCACATCAGCTGGAGATTAACGACACAAACCGGTCACAAACTCCCGGG 255
QY 1016 ACACCCAGGAGTGGCCCTTAGAAAAAGCCAAAGTGTCTGAAAAATTTATCAGTTTCTTACA 1075
DB 254 ACACCCAGGAGTGGCCCTTAGAAAAAGCCAAAGTGTCTGAAAAATTTATCAGTTTCTTACA 195
QY 1076 AGCACAACTCTCATCTTCGACACTTTGCTCTACTAGAGAGCGCCA-GAGAGGAGG 1134
DB 194 AGCACAACTCTCATCTTCGACACTTTGCTCTACTAGAGAGCGCCAGGAGGAGG 135
QY 1135 AGTGTGGCCAGGAGGACGACAGTGCAGAACAAACAAATGAGGCGCAACAGTTTCTTAC 1194
DB 134 AGTGTGGCCAGGAGGAGGAGTGCAGAACAAACAAATGAGGCGCAACAGTTTCTTAC 75
QY 1195 ATGTTCTAACGTTTGACTTTTGAACACAGTTTAAACACAGTGTGCTTGGTCAGCTCCAGTG 1254
DB 74 ATGTTCTAACGTTTGACTTTTGAACACAGTTTAAACACAGTGTGCTTGGTCAGCTCCAGTG 15
QY 1255 TGTCGTCCTGGG 1268
DB 14 TGTCGTCCTGGG 1

RESULT 14
AJ449334 688 bp mRNA linear EST 19-APR-2002
LOCUS
DEFINITION
AJ449334 riken1 Gallus gallus cDNA clone 21k24r1, mRNA sequence.
ACCESSION
AJ449334
VERSION
AJ449334.1 GI:20216555
KEYWORDS
EST.

SOURCE
chicken.
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 688).

REFERENCE
AUTHORS
Buerstedde, J.M.
TITLE
Gallus gallus bursal lymphocyte EST
JOURNAL
Unpublished (2002)
COMMENT
Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany

Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES
source
1. .688
/location/Qualifiers
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="21k24r1"
/clone_lib="riken1"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
BASE COUNT 206 a 156 c 157 g 169 t
ORIGIN

Query Match 23.8%; Score 483.6; DB 1; Length 688;
Best Local Similarity 82.5%; Pred. No. 1.8e-112;
Matches 566; Conservative 0; Mismatches 119; Indels 1; Gaps 1;
QY 440 CGCAGTATCAGAGCCCTCAGCAGCCACCCAGACCCGCTGGGTGGCCACGCAACAGAA 499
DB 2 CACAGTATCAGAGCCCTCAACAGCCACCCCAAAATCGCTGGATTGCTTCGCAACAGAA 61
QY 500 ACCCGCGCTTTGGCAGAGCGAGGGGCTGGCAGCGATAGCAACTCTCTGGAAAGCTCC 559
DB 62 ATCAGCTTTTGGCCAAAGTGGAGGAACCTGGTAATGACAGCAATTCAGCTGGCAGTACC 121
QY 560 AGCTTAATTCTGCCCCAGCGTCGAATCCACCCCGCTCTTGAATAAAGTGAAGGCTGCTC 619
DB 122 AGCTTAACCTGTTCCAAAGTGGTGGTCCCATCTCTGTTCTTGAATAAAGTGAAGGCTGCTC 181
QY 620 ACAGCTACACCCGAAAGAGTTTGTAGTGGATCTGAAGAGCGGGCTGTGTTTCATCATCA 679
DB 182 ACAGCTATTAATCTCAAGATTTTGAATGGAACCTTAAATAATGAGCGTGTGTTTCAATAA 241
QY 680 AGAGCTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCCATCTGGTGTAGCACAG 739
DB 242 AGAGCTATTCTGAGGATGATATTCATCGTTCCATTAAGTATTCTATTGTTGTAGTACG 301
QY 740 AGCAGCGCAACAGCGCTGGACAGCGCTTCCGCTGTCATAGCAGCAAGCGGCCGCTCT 799
DB 302 AGCATGGCAACAAACGCTGGACAGTGTCTTCCGTCCATGATAGCAAGGCTCCGCTCT 361
QY 800 ACTGCTCTTCACGCTCAATGGAGTGGGCAATTTTGTGGGTGGCGGAGATCAAGTCCC 859
DB 362 ACTGCTCTTCAGTGTCAATGGCAGTGGACACTTCTGTGGAGTTGACAGATGAAATCAC 421
QY 860 CCGTGGACTACGGCACAGTCCCGGGGTCTGGTCTCAGGACAAAGTGGAGGGAAAGTTTG 919
DB 422 CTGTGGACTATGSCACAGTGCAGGTGTCTGTCTCAGGACAAAGTGGAGGGGAAATTTG 481
QY 920 ATGTCAGTGGATTTTGTAAAGGATGTACCCAAATTAACAGCTCCGGCAGCATCAGGCTGG 979
DB 482 ATGTCAAGTGGATCTTTGTGAAGGATGTGCCCAACAAACAGCTCCGACACATCAGGCTGG 541
QY 980 AGAATACGACAAACAAACCGGTCACAAACT-CCGGGACACCCAGGAGTGGCTTTAGAA 1038
DB 542 AGAACAATGACAAACAAACCTGTTACAAACTCCCGGTGACACAGAGGAGTGCCTTTAGAA 601
QY 1039 AAAGCCAAGCAAGTGTGAAAAATTTATCAGTTCTCTACAGCACACAACTCCATCTTCGAC 1098
DB 602 AAAGCAAAACAGTGTCTTAAATTTATGTTACTTACAGCACACAGCTCCATCTTTGAT 661
QY 1099 GACTTTGCTCCTACGAGAGCGCCA 1124
DB 662 GACTTTTCTCATTTATGAAAGCGCCA 687

RESULT 15
AW387916/c
LOCUS
DEFINITION
MR4-ST0119-071099-010-F04 ST0119 Homo sapiens cDNA, mRNA sequence.
ACCESSION
AW387916
VERSION
AW387916.1 GI:6892575
KEYWORDS
EST.

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 499)
TITLE HCGP <http://www.ludwig.org.br/ORESTES>.
JOURNAL The FAPESP/LICR Human Cancer Genome Project
COMMENT Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR4&t2=MR4-ST0119-071059-010-F04&t3=1999-10-07&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 465.
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1. 499
Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="ST0119"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 103 a 144 c 118 g 134 t
ORIGIN
Query Match 23.7%; Score 480.6; DB 2; Length 499;
Best Local Similarity 99.0%; Pred. No. 9.8e-112;
Matches 494; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 777 CATGACGACGAGGGCCCGTCTACTGCTCTTACGCTCAATGGAGTGGGCAATTTTG 836
Db 499 CATGACGACGAGGGCCCGTCTACTGCTCTTACGCTCAATGGAGTGGGCAATTTTG 440
QY 837 TGGGGTGGCGGAGTAACTCCCGTGGACTACGACGAGTCCGGGTCTGCTCTCA 896
Db 439 TGGGGTGGCGGAGTAACTCCCGTGGACTACGACGAGTCCGGGTCTGCTCTCA 380
QY 897 GCACAAAGTGGAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGATGTACCCCAATAA 956
Db 379 GCACAAAGTGGAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGATGTACCCCAATAA 320
QY 957 CCAGTCTCCGCGCATCAGGCTGGAGAAATACGACAAACACCGGTCAAAATCCCGGGA 1016
Db 319 CCAGTCTCCGCGCATCAGGCTGGAGAAATACGACAAACACCGGTCAAAATCCCGGGA 260
QY 1017 CACCCAGGAGGTGCCCTTAGAAAACCAAGCAAGTCTGAAAATATCAGTTCCTACAA 1076
Db 259 CACCCAGGAGGTGCCCTTAGAAAACCAAGCAAGTCTGAAAATATCAGTTCCTACAA 200
QY 1077 GCACAAACTCCACTCTTCGACGACTTGTCTACTACGAGAGAGCGCA - GAGGAGGAGGA 1135
Db 199 GCACAAACTCCACTCTTCGACGACTTGTCTACTACGAGAGAGCGCAAGGAGGAGGA 140
QY 1136 GGTGGTGCAGGAAGACGGCAGAGTGCAGAAACCAACCAATGAGGCGCAACCAAGTTTCTTACA 1195
Db 139 GGTGGTGCAGGAAGACGGCAGAGTGCAGAAACCAACCAATGAGGCGCAACCAAGTTTCTTACA 80
QY 1196 TGTTCTAAAGCTTTGACTTTGAAAACAGTTTAAACACGTTGGTCTGGTCCAGTCCAGTGT 1255
Db 79 TGTTCTAAAGCTTTGACTTTGAAAACAGTTTAAACACGTTGGTGAATGTTGAGTCCAGTGT 20

QY 1256 GTCGTCCCGTCCGGGGGTT 1274
Db 19 GTCGTCCCGTCCGGGGGTT 1
RESULT 16
AW387858/c 584 bp mRNA linear EST 04-FEB-2000
LOCUS MR4-ST0118-151299-023-b10 ST0118 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW387858
ACCESSION AW387858
VERSION AW387858.1 GI:6892517
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 584)
TITLE HCGP <http://www.ludwig.org.br/ORESTES>.
JOURNAL The FAPESP/LICR Human Cancer Genome Project
COMMENT Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR4&t2=MR4-ST0118-151299-023-b10&t3=1999-12-15&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 496.
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1. 584
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0118"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 121 a 161 c 151 g 151 t
ORIGIN

Query Match 23.0%; Score 466.8; DB 2; Length 584;
Best Local Similarity 92.9%; Pred. No. 3.3e-108;
Matches 522; Conservative 0; Mismatches 37; Indels 3; Gaps 3;
QY 707 GCTCCATTAAAGTACTCCATCTGGTGTAGCAGACGACGCAAGCGCTTGGACAGCG 766
Db 561 GCACCTCCATTAACTCTCTGCTGTAGCAGCAGTCACGCGCACAGCGCTTGGAAAGCGC 502
QY 767 CCTTCGGTGCATGAGCAGCAAGGGGCCGCTCTACTGCTTTCAGCGTCAATGGAGTG 826
Db 501 CTTCCCTGGCATGAGCAGCAA - GGGCCCGCTCTACTGCTCTTACGCGCTCAATGGAGTG 443
QY 827 GGCATTTTGTGGGTGGCCGAGATGAAGTCCCGTGGACTACGCGCACCGTCCGGGG 886
Db 442 GGCATTTTGTGGGTGGCCGAGATGAAGTCCCGTGGACTACGCGCACCGTCCGGGG 383
QY 887 TCTGCTCTCAGGACAAGTGGAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGGATG 946
Db 382 TCTGCTCTCAGGACAAGTGGAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGGATG 323
QY 947 TACCAATAACCAAGTCCGGCAATCAGCGTGGAGAAATAACGACAAACCAACCGGTCCAAA 1006
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Db 322 TACCCATACAGCTCCGGCAGCATCAGGCTGGAGAAATACGACACAAACCGGTACAG 263
QY 1007 ACTCCGGGACACCCAGGAGTGCCTTTAGAAAAAGCC-AAGCAAGTGCCTGAAAAATTATC 1065
Db 262 ACTCCGGGACACCCAGGAGTGCCTTTAGAAAAAGCCAAAGCAAGTGCCTGAAAAATTATC 203
QY 1066 AGTTCCTACAGCACACAACTCATCTTCGACGACTTTGCTCCTACACGAGAGAGCGCCA- 1124
Db 202 AGTTCCTACAGCACACAACTCATCTTCGACGACTTTGCTCCTACACGAGAGAGCGCCAG 143
QY 1125 GAGGAGGAGAGTGGTGGCCAGGACGCGAGAGTGAACAAACAACTAGGCGGCAACC 1184
Db 142 GAGGAGGAGAGTGGTGGCCAGGACGCGAGAGTGAACAAACAACTAGGCGGCAACC 83
QY 1185 AGTTCCTACAGTCTTAAGCTTTGACTTTTGAACAAAGTTTTAAACACAGTTCGCTGGTC 1244
Db 82 AGTTCCTACAGTCTTAAGCTTTGACTTTTGAACAAACAGTTCGCTGGTC 23
QY 1245 AGTCCAGTGTGCTGCTCGG 1266
Db 22 AGTCCAGTGTGCTGCTCGG 1

RESULT 17
AA976117
LOCUS on33b10.s1 NCI_CGAP_Lus Homo sapiens cDNA clone IMAGE:1558459 3',
DEFINITION mRNA sequence.
ACCESSION AA976117
VERSION AA976117.1 GI:3151909
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 460)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@imail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 439.
Location/Qualifiers
1. 460
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/clone_lib="NCI_CGAP_Lus"
/tissue_type="carcinoid"
/lab_host="DHI08"
/notes="Organ: lung; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p773 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
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BASE COUNT 123 a 78 c 79 g 180 t

Query Match 22.5%; Score 456.8; DB 1; Length 460;

Best Local Similarity 99.6%; Pred. No. 1.1e-105;

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Matches 458; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1402 TATCAATCAGACTGATCTAATGTGAAATGTAAAGTATCTCTTAAAAACAAAGCATCTATTTT 1461
Db 1 TATCAATCAGACTGATCTAATGTGAAATGTAAAGTATCTCTTAAAAACAAAGCATCTATTTT 60
QY 1462 GGAGAAAAATGTGTTCTTAAATTCAGTCAATTTGATATTTCTGTGAGACTTCATATTTCTCA 1521
Db 61 GGAGAAAAATGTGTTCTTAAATTCAGTCAATTTGATATTTCTGTGAGACTTCATATTTCTCA 120
QY 1522 TCCCTTTATTTGCTTTTATAGCAACATAAGAAACCATGAGTCAATTTTGTGATTTAGAGTAT 1581
Db 121 TCCCTTTATTTGCTTTTATAGCAACATAAGAAACCATGAGTCAATTTTGTGATTTAGAGTAT 180
QY 1582 TCTGATAAAATCTCTTGAATACTGAAATCAAAAGGTTAATGATTTTGTTCATTCTG 1641
Db 181 TCTGATAAAATCTCTTGAATACTGAAATCAAAAGGTTAATGATTTTGTTCATTCTG 240
QY 1642 ATTTGTCAATTTTATTAATCTGTTATCGGTCTAAAGTCTTAATTTACCATTTGATTTTCT 1701
Db 241 ATTTGTCAATTTTATTAATCTGTTATCGGTCTAAAGTCTTAATTTACCATTTGATTTTCT 300
QY 1702 GCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTGTGTTTTTGTGAAA 1761
Db 301 GCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTGTGTTTTTGTGAAA 360
QY 1762 ATCTTTCCCTCCAGATCTGTGCCCACCTGAACAGCCCGCTCCCTCAGTGTCTCTGTGT 1821
Db 361 ATCTTTCCCTCCAGATCTGTGCCCACCTGAACAGCCCGCTCCCTCAGTGTCTCTGTGT 420
QY 1822 CCGATTGGGCTGATGCTGTGTTGGGGCATGATGTGTGGAGG 1861
Db 421 CCGATTGGGCTGATGCTGTGTTGGGGCATGATGTGTGGAGG 460

RESULT 18
AL580786
LOCUS AL580786 LTI_NFL008.TC2 Homo sapiens cDNA clone CS0DJ014YN09 5
DEFINITION prime, mRNA sequence.
ACCESSION AL580786
VERSION AL580786.1 GI:12947147
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 778)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 778
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DJ014YN09"
/clone_lib="LTI_NFL008.TC2"
/sex="male"
/tissue_type="T cells from T cell leukemia"
/notes="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
```


Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone.
This read has been verified (found to hit its original self in the
correct orientation)

MGI:209275
Seq primer: -40RP from Gibco
High quality sequence stop: 463
POLYA=No.

FEATURES
source Location/Qualifiers
1. 614
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="IMAGE:318659"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: pRT3D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTCAAGTGGGCGCGCATTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT3D vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."

BASE COUNT 169 a 136 c 163 g 144 t 2 others
ORIGIN

Query Match 21.8%; Score 442.4; DB 1; Length 614;
Best Local Similarity 86.3%; Pred. No. 5.5e-102;
Matches 499; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

QY 667 GTGTTTCATCATCAAGAGCTACTCTGAGACGACATCCACCGCTCCATTAAGTACTCCATC 726
Db 2 GTGTTTCATCATCAAGAGCTATTCTGAGGACGACATCCACCGCTCCATCAAGTACTCCATC 61

QY 727 TGGTGTAGCAGACGACGCGCAACAGCGCTGACAGCGCTTCCGCTGCATGAGCAGC 786
Db 62 TGGTGTAGTACTGAACACGCGCAACAGCGCTGACAGCGCTTCCGCTCCATGAGCAGC 121

QY 787 AAGGGGCGCGTCTACCTGCTCTTCCAGGCTCAATGGGAGTGGGCAATTTTGTGGGTGGCC 846
Db 122 AAGGGGCGCTGTTATCTCTCTTCCAGTGTCAATGGGAGTGGCAATTTTGTGGGTGGCA 181

QY 847 GAGATGAAGTCCCCCGTGGACTACGGACACGATGTCGGGGTCTGGTCTCAGGACAAGTGG 906
Db 182 GAGATGAAGTCCCCGTGGACTACGGACACGATGTCGGGGTCTGGTCTCAGGACAAGTGG 241

QY 907 AAGGGGAGTTTGTATGTCAGTGGATTTTGTGAAGATGTACCAATACAGCTCCGG 966
Db 242 AAGGGGAGTTTGTATGTTGAAGTGGATTTTGTGAAGATGTGCGCAACACCAAGTCCGG 301

QY 967 CACATCAGGCTGAGATAACGACAAACAAACCTCCCGGACACCCAGGAG 1026
Db 302 CACATCAGACTGGAGATACGACAAACAAACCTGTCAAACTCTCCGTGATACAGGAG 361

QY 1027 GTGCCCTTAGAAAAAGCAAGAGTCTGAAATATTCAGTTTCTTACAAGCACACAACC 1086
Db 362 GTGCCCTTAGAAAAAGCAAAAGTCTGAAGATATTATCGTCTCTTATAAGCACACAACC 421

QY 1087 TCCATCTTCACGACNTTGTCTACTAGACAGCGCCA-GAGGAGGAGGAGTGGTGGC 1145

Db 422 TCTATCTTTGACGACTTTTCTCATTTATGAGAGCCCGAGGAGGAGGTGGTGGT 481

QY 1146 AAGGAACGGCAGAGTTCGAAACAAACATGAGGCGGACACCAAGTCTTCTTACATGTCTTAACG 1205

Db 482 AAGGAACGAGAGTTCGAAACAAACATGAGGCGGACACCAAGTCTTCTTACATGTCTTAACG 541

QY 1206 TTTGACTTTTGAACACAGTCTTAAACACAGTGTGTCTTGGT 1243

Db 542 TGACTTNTGAAAACAGAGTTNTAAAGCTGTATGTGTGT 579

RESULT 21
AI083909/c
LOCUS
DEFINITION
qf26b05.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:1751121 3',
similar to TR:044503 004503 SEQUENCE OF BAC F21M12 FROM ARABIDOPSIS
THALIANA CHROMOSOME 1, COMPLETE SEQUENCE. ; mRNA sequence.

ACCESSION AI083909
VERSION AI083909.1 GI:3422332
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 449)
REFERENCE
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/RTGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/hbrp/image/image.html
Insert length: 1946 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 418.

FEATURES
source Location/Qualifiers
1. 449
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:1751121"
/issue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: brain; Vector: pRT3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTCAAGTGGGCGCGCATTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRT3D vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 120 a 106 c 100 g 123 t
ORIGIN

Query Match 20.9%; Score 423.4; DB 1; Length 449;
Best Local Similarity 99.3%; Pred. No. 3.4e-97;
Matches 446; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 960 GCTCCGGCACATCAGGCTGGAGATTAACGACAAACCGGTCAAACTCCCGGACAC 1019
Db 449 GCTCCGGCACATCAGGCTGGAGATTAACGACAAACCGGTCAAACTCCCGGACAC 390

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QY 1020 CCAGAGGTGCCCTTAGAAAAAGCCAGCAAGTGTCTGAAAAATTATCAGTTCTCTACAAGCA 1079
Db 389 CCAGGAGGTGCCCTTAGAAAAAGCCAGCAAGTGTCTGAAAAATTATCAGTTCTCTACAAGCA 330
QY 1080 CACAACCTCCATCTTCGACGACTTTGCTCCTCCTACGAGAGCGCCA-GAGGAGGAGAGGT 1138
Db 329 CACAACCTCCATCTTCGACGACTTTGCTCCTCCTACGAGAGCGCCA-GAGGAGGAGAGAGGT 270
QY 1139 GGTGGCAGAGAACCGCAGAGTCGAAACAAACAAATGAGGGCGAAACAGTTTCTTACATGT 1198
Db 269 GGTGGCAGAGAACCGCAGAGTCGAAACAAACAAATGAGGGCGAAACAGTTTCTTACATGT 210
QY 1199 TCTAACGTTTGACTTTGAAAAACAGTTTAAAAACAGTGTCTGCTGCTCAGCTCCAGTGTGTC 1258
Db 209 TCTAACGTTTGACTTTGAAAAACAGTTTAAAAACAGTGTCTGCTGCTCAGCTCCAGTGTGTC 150
QY 1259 GTCCCGTGGGGGGTGTAGTGTGTCATCTTCTGCTTCTTCTGCTGTTGATTTTGGCCACA 1318
Db 149 GTCCCGTGGGGGGTGTAGTGTGTCATCTTCTGCTTCTTCTGCTGTTGATTTTGGCCACA 90
QY 1319 TGGATCTGCATTTATTTGTACTTTTCTATGTATTATAATCTCTAGAAAGTCACTAATAA 1378
Db 89 TGGATCTGCATTTATTTGTACTTTTCTATGTATTATAATCTCTAGAAAGTCACTAATAA 30
QY 1379 AGGAGTATTTTTTTTGTGAGCTTATCAA 1407
Db 29 AGGAGTA-TTCTTTTGTGAGCTTATCAA 2

RESULT 22
LOCUS AW387755/c
DEFINITION MR4-ST0118-041099-010-A06 ST0118 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW387755
VERSION AW387755.1 GI:6892414
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC0&t2=MR4-ST0118-041099-010-A06&t3=1999-10-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 434.
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    Location/Qualifiers
        1..435
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="ST0118"
            /dev_stage="Adult"
            /note="Organ: stomach; Vector: puc18; Site: 1: SmaI;
            Site: 2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the pUC 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
        90 a 121 c 104 g 120 t

BASE COUNT
ORIGIN
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Query Match 20.6%; Score 418.2; DB 2; Length 435;
Best Local Similarity 99.1%; Pred. No. 7.2e-96;
Matches 431; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 841 GTGCCGAGATGAAGTCCCGTGGACTACCGCACAGTCCGGGGTCTGGTCTCAGGAC 900
Db 435 GTGCCGAGATGAAGTCCCGTGGACTACCGCACAGTCCGGGGTCTGGTCTCAGGAC 376
QY 901 AAGTGGAAAGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGGATGTACCCCAATACCAG 960
Db 375 AAGTGGAAAGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGGATGTACCCCAATACCAG 316
QY 961 CTCGGGCATCATCAGCTGGAGAAATACGACAAACAAACCGGTCAAAAACCTCCGGGACACC 1020
Db 315 CTCGAGCATCATCAGCTGGAGAAATACGACAAACAAACCGGTCAAAAACCTCCGGGACACC 256
QY 1021 CAGGAGGTGCCCTTAGAAAAAGCCAAAGTGTCTGAAAAATTTATCAGTTTCTTACATGTT 1080
Db 255 CAGGAGGTGCCCTTAGAAAAAGCCCTAGCAAGTGTCTGAAAAATTTATCAGTTTCTTACATGTT 196
QY 1081 ACAACCTCCATCTTCGACGACTTTTCTCTACCTACGAGAAAGCGCCA-GAGGAGGAGGAGTG 1139
Db 195 ACAACCTCCATCTTCGACGACTTTTCTCTACCTACGAGAAAGCGCCAGGAGGAGGAGTG 136
QY 1140 GTGCCAAAGGAACGGCAGAGTCGAAAAACAAATCAGGCGCAACAGTTTCTTACATGTT 1199
Db 135 GTGCCAAAGGAACGGCAGAGTCGAAAAACAAATCAGGCGCAACAGTTTCTTACATGTT 76
QY 1200 CTAACTGTTGACTTTGAAACAGTTTAAACACAGTCTGCTGGTCCAGTCCAGTCTGTGCG 1259
Db 75 CTAACTGTTGACTTTGAAACAGTTTAAACACAGTCTGCTGGTCCAGTCCAGTCTGTGCG 16
QY 1260 TCCCGTGGGGGGTT 1274
Db 15 TCCCGTGGGGGGTT 1

RESULT 23
LOCUS AV725141
DEFINITION AV725141 HTC Homo sapiens cDNA clone HTCMH07 5', mRNA sequence.
ACCESSION AV725141
VERSION AV725141.1 GI:10830231
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 429)
AUTHORS Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu
S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA HTC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
    Location/Qualifiers
        1..429
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="HTCMH07"
            /clone_lib="HTC"
            /tissue_type="Hypothalamus"
            /dev_stage="Adult"
            /lab_host="SOLR"
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/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 125 a 59 c 57 g 188 t
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Query Match 20.6%; Score 418; DB 2; Length 429;
Best Local Similarity 99.8%; Pred. No. 8.1e-96;
Matches 429; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1329 TTTATTGTACTTTTCTATGTAATTAATCCTGTAGAAGTCACTAATAAGGAGTATTT 1388
DB 1 TTTATTGTACTTTTCTATGTAATTAATCCTGTAGAAGTCACTAATAAGGAGTATTT 59
QY 1389 TTTTGTGACGCTTATCAATCAGACTGATCTAATGTAAGTATCCTTAAAAACA 1448
DB 60 TTTTGTGACGCTTATCAATCAGACTGATCTAATGTAAGTATCCTTAAAAACA 119
QY 1449 AAGCATCTATTTGGCGAAGAAATGTGTTCTTAAATTCAGTCATTTGCGAGAC 1508
DB 120 AAGCATCTATTTGGCGAAGAAATGTGTTCTTAAATTCAGTCATTTGCGAGAC 179
QY 1509 TCCATATTTCTCATCCCTTTATGCTTTTAGCAAACTACTGAAATGTAAGTATTTG 1568
DB 180 TCCATATTTCTCATCCCTTTATGCTTTTAGCAAACTACTGAAATGTAAGTATTTG 239
QY 1569 TCATTTAGAGTATTTCTGATAAAATCTCTGAAATCTGAAATCTAATGATTT 1628
DB 240 TCATTTAGAGTATTTCTGATAAAATCTCTGAAATCTGAAATCTAATGATTT 299
QY 1629 TTTGTCATTTCTGATTTGTCATTTTATATCTGTTATCGGTCTAAAGTCTAATACCC 1688
DB 300 TTTGTCATTTCTGATTTGTCATTTTATATCTGTTATCGGTCTAAAGTCTAATACCC 359
QY 1689 ATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGCGACACTTTTTT 1748
DB 360 ATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGCGACACTTTTTT 419
QY 1749 TTTTATTTTG 1758
DB 420 TTTTATTTTG 429
RESULT 24
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LOCUS AV729447 HTC Homo sapiens cDNA clone HTCAMP05 5', mRNA sequence.
DEFINITION AV729447
ACCESSION AV729447
VERSION AV729447.1 GI:10838868
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 429)
AUTHORS Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu
S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Shen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA HTC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. .429
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTCAMP05"
FEATURES
Source
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/clone_lib="HTC"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 125 a 59 c 57 g 188 t
ORIGIN
Query Match 20.6%; Score 418; DB 2; Length 429;
Best Local Similarity 99.8%; Pred. No. 8.1e-96;
Matches 429; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1329 TTTATTGTACTTTTCTATGTAATTAATCCTGTAGAAGTCACTAATAAGGAGTATTT 1388
DB 1 TTTATTGTACTTTTCTATGTAATTAATCCTGTAGAAGTCACTAATAAGGAGTATTT 59
QY 1389 TTTTGTGACGCTTATCAATCAGACTGATCTAATGTAAGTATCCTTAAAAACA 1448
DB 60 TTTTGTGACGCTTATCAATCAGACTGATCTAATGTAAGTATCCTTAAAAACA 119
QY 1449 AAGCATCTATTTGGCGAAGAAATGTGTTCTTAAATTCAGTCATTTGCGAGAC 1508
DB 120 AAGCATCTATTTGGCGAAGAAATGTGTTCTTAAATTCAGTCATTTGCGAGAC 179
QY 1509 TCCATATTTCTCATCCCTTTATGCTTTTAGCAAACTACTGAAATGTAAGTATTTG 1568
DB 180 TCCATATTTCTCATCCCTTTATGCTTTTAGCAAACTACTGAAATGTAAGTATTTG 239
QY 1569 TCATTTAGAGTATTTCTGATAAAATCTCTGAAATCTGAAATCTAATGATTT 1628
DB 240 TCATTTAGAGTATTTCTGATAAAATCTCTGAAATCTGAAATCTAATGATTT 299
QY 1629 TTTGTCATTTCTGATTTGTCATTTTATATCTGTTATCGGTCTAAAGTCTAATACCC 1688
DB 300 TTTGTCATTTCTGATTTGTCATTTTATATCTGTTATCGGTCTAAAGTCTAATACCC 359
QY 1689 ATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGCGACACTTTTTT 1748
DB 360 ATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGCGACACTTTTTT 419
QY 1749 TTTTATTTTG 1758
DB 420 TTTTATTTTG 429
RESULT 25
AV729585 429 bp mRNA linear EST 17-OCT-2000
LOCUS AV729585 HTC Homo sapiens cDNA clone HTCANC06 5', mRNA sequence.
DEFINITION AV729585
ACCESSION AV729585
VERSION AV729585.1 GI:10839006
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 429)
AUTHORS Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu
S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Shen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA HTC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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source 1..429
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HTCCAN06"
/clone_lib="HTC"
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/dev_stage="Adult"
/lab_host="SOLR"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 125 a 59 c 57 g 188 t
ORIGIN
Query Match 20.6%; Score 418; DB 2; Length 429;
Best Local Similarity 99.8%; Pred. No. 8.1e-96;
Matches 429; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1329 TTTATTGTACTTTTCTATGATTAATATCCCTGTAGAGTCACCTAATAAGGAGTATTT 1388
Db 1 TTTATTGTACTTTTCTATGATTAATATCCCTGTAGAGTCACCTAATAAGGAGTA-TT 59
QY 1389 TTTTGTGTCAGCTTATCAATCAGACTGATCTAATGTGAATGTAAAGTATCCTTAAAAACA 1448
Db 60 TTTTGTGTCAGCTTATCAATCAGACTGATCTAATGTGAATGTAAAGTATCCTTAAAAACA 119
QY 1449 AAGCATCTATTTGGCAGAAATGTGTTCTTAAATTCAGTCAATTCGATATTCGTGAGAC 1508
Db 120 AAGCATCTATTTGGCAGAAATGTGTTCTTAAATTCAGTCAATTCGATATTCGTGAGAC 179
QY 1509 TTCAATATTTCTCATCCCTTATTCCTTTTAGCAACATAAGAAACCATGATCTTTTG 1568
Db 180 TTCAATATTTCTCATCCCTTATTCCTTTTAGCAACATAAGAAACCATGATCTTTTG 239
QY 1569 TCATTTAGAGTATTCGATAAAATCTCTGAAATCTGAAATCAAAAGGTTAATCATTT 1628
Db 240 TCATTTAGAGTATTCGATAAAATCTCTGAAATCTGAAATCAAAAGGTTAATCATTT 299
QY 1629 TTTGTTCAATCTGATTTGTCATTTATTAATCTGTTATCGGTCCTAAAGTGCTAATTTACCC 1688
Db 300 TTTGTTCAATCTGATTTGTCATTTATTAATCTGTTATCGGTCCTAAAGTGCTAATTTACCC 359
QY 1689 ATTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAATTTGGCAGACACTTTT 1748
Db 360 ATTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAATTTGGCAGACACTTTT 419
QY 1749 TTTTTTTTTG 1758
Db 420 TTTTTTTTTG 429

RESULT 26
AV747364
LOCUS AV747364 NPC Homo sapiens cDNA clone NPCKE10 5', mRNA sequence.
DEFINITION AV747364
ACCESSION AV747364.1 GI:10905212
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 548)
REFERENCE
AUTHORS Song,H., Peng,Y., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N.,
Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu
,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Ye,M., Zhang,Q.,
Han,Z., Chen,Z., Hu,R. and Chen,J.
Homo sapiens NPC library cDNA clones
Unpublished (2000)
Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045(ex.663332)
Fax: 86-21-64743206

Email: mbsh@ms.stn.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
Location/Qualifiers
1..548
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NPCKE10"
/clone_lib="NPC"
/tissue_type="pituitary"
/dev_stage="Adult"
/lab_host="SOLR"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 149 a 118 c 127 g 143 t 11 others
ORIGIN
Query Match 20.0%; Score 406.6; DB 2; Length 548;
Best Local Similarity 91.0%; Pred. No. 6.9e-93;
Matches 483; Conservative 0; Mismatches 42; Indels 6; Gaps 5;
QY 915 GTTTCATGTCCTCAGTCGATTTTGTAAAGATGTACCCATACACAGCTCCCGGCACATCAG 974
Db 1 GGTTCATGTCCTCAGTCGAGGCTTTNACAGGCACACCTCTCAGCAAGGCCCGCGGATGAACAG 60
QY 975 GCTGAGAGTAATACGACAAACACCGGTCAAACTCCCGGGACACCCAGAGAGTGCCCTT 1034
Db 61 CTGAGAGTAATACGACAAACACCGGTCAAACTCCCGGGACACCCAGAGAGTGCCCTT 120
QY 1035 AGAAAAAGCCAAAGCAAGTCTCGAAAATTTATCAGTTCTTACAAAGCACAACTCCATCTT 1094
Db 121 AGAAAAAGCCAAAGCAAGTCTCGAAAATTTATCAGTTCTTACAAAGCACAACTCCATCTT 180
QY 1095 CGACGACTTGTCTACTAGAGAGCGGCA-CAGGAGGAGGAGTGGTCCGCAAGAACG 1153
Db 181 CGACGACTTGTCTACTAGAGAGCGGCAAGGAGGAGGAGTGGTCCGCAAGAACG 240
QY 1154 GCAGAGTCCGAAACAAACAAATGAGGCGCAACAGTTTCTTACATGTTCTAAACGTTTGACTT 1213
Db 241 GNAAGTCNAACAAACAAATGAGGCGCAACAGTTTCTTACATGTTCTAAACGTTTGACTT 300
QY 1214 TGAAACACAGTTTAAACACAGTGTGTTGTCAGCTCCAGTGTGTCGTCGCCGGGGT 1273
Db 301 TGAAACACAGTTTAAACACAGTGTGTTGTCAGCTCCAGTGTGTCG-CGCCGCGGGGT 359
QY 1274 TGAGTGTGTCATCTTTGCCCTTTCTTGTGTTGATTTTGGCCAGATGGATCTGCATTAT 1333
Db 360 TGAGTGTGTCATCTTTGCCCTTTCTTGTGTCATGA-TTTTGGCCAGATGGATCTGCATTAT 418
QY 1334 TTGTACTTTTCTATGATTAATAATCCTGTAGAGTCACCTAATAAGGAGTATTTTTTTT 1393
Db 419 TTGTAC-TTTTCTATGATTAATAATCCTGTAGAGTCACCTAATAAGGAGTATTTTTTTT 477
QY 1394 TGTGAGCTTATCAATCAGACTGATCTAATGTGAATGTAAAGTATCCTTAAA 1444
Db 478 --GCAGCTTATCAATCAGACTGATCTAATGTGAATGTAAAGTATCCTTAAA 526

RESULT 27
AL550164
LOCUS AL550164 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI040YK06 5
DEFINITION AL550164
ACCESSION AL550164
VERSION AL550164.1 GI:12886868
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1053)
REFERENCE
AUTHORS Song,H., Peng,Y., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N.,
Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu
,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Ye,M., Zhang,Q.,
Han,Z., Chen,Z., Hu,R. and Chen,J.
Homo sapiens NPC library cDNA clones
Unpublished (2000)
Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
```

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 1053
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1040YK06"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 198 a 349 c 314 g 191 t 1 others
ORIGIN

Query Match 20.0%; Score 405.8; DB 1; Length 1053;
Best Local Similarity 98.3%; Pred. No. 1.3e-92;
Matches 410; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAAAGGACAAAGTAAATAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 60
DB 366 CAAAGGACAAAGTAAATAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 425

QY 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATTCAGAGTAACAGTTACCCCTCAA 120
DB 426 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATTCAGAGTAACAGTTACCCCTCAA 485

QY 121 TGAGCGACCCCTACTCTGTCAGCTATTACCGCGCTCCATTTGGATTTCTTACTCCCTCA 180
DB 486 TGAGCGACCCCTACTCTGTCAGCTATTACCGCGCTCCATTTGGATTTCTTACTCCCTCA 545

QY 181 ATGAGGCTCCGTGCTTACTGCGAGGACCCCTCCGATTCATCTCACCACCTACGGAC 240
DB 546 ATGAGGCTCCGTGCTTACTGCGAGGACCCCTCCGATTCATCTCACCACCTACGGAC 605

QY 241 AGCTCAGTAACGGAGACCATCATTTTATGACGATGCTGTTTTGGCAGCCTGGGGGCC 300
DB 606 AGCTCAGTAACGGAGACCATCATTTTATGACGATGCTGTTTTGGCAGCCTGGGGGCC 665

QY 301 TGGGGAACAACATCTATCAGCACAGTTCAATTTTTTCCCTGAAAACCCCTGCGTTCTCAG 360
DB 666 TGGGGAACAACATCTATCAGCACAGTTCAATTTTTTCCCTGAAAACCCCTGCGTTCTCAG 725

QY 361 CATGGGGGACAAAGTGGTCTCAAGGTGAGGACCCAGAGCTCAGCCTCTCCAGCA 417
DB 726 CATGGGGGACAAAGTGGTCTCAAGGTGAGGACCCAGAGCTCAGCCTCTCCAGCA 782

RESULT 28
AL514504
LOCUS
DEFINITION AL514504 LTI_NFL006_PL2 Homo sapiens cDNA clone CLOBB003ZF07 5
prime, mRNA sequence.
ACCESSION AL514504
VERSION AL514504.1 GI:12777998
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 977)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 977
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CLOBB003ZF07"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 191 a 310 c 284 g 181 t 11 others
ORIGIN

Query Match 19.8%; Score 402.2; DB 1; Length 977;
Best Local Similarity 96.2%; Pred. No. 1.1e-91;
Matches 401; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAAAGGACAAAGTAAATAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 60
DB 270 CAAAGGACAAAGTAAATAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 329

QY 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATTCAGAGTAACAGTTACCCCTCAA 120
DB 330 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATTCAGAGTAACAGTTACCCCTCAA 389

QY 121 TGAGCGACCCCTACTCTGTCAGCTATTACCGCGCTCCATTTGGATTTCTTACTCCCTCA 180
DB 390 TGAGCGACCCCTACTCTGTCAGCTATTACCGCGCTCCATTTGGATTTCTTACTCCCTCA 449

QY 181 ATGAGGCTCCGTGCTTACTGCGAGGACCCCTCCGATTCATCTCACCACCTACGGAC 240
DB 450 ATGAGGCTCCGTGCTTACTGCGAGGACCCCTCCGATTCATCTCACCACCTACGGAC 509

QY 241 AGCTCAGTAACGGAGACCATCATTTTATGACGATGCTGTTTTGGCAGCCTGGGGGCC 300
DB 510 AGCTCAGTAACGGAGACCATCATTTTATGACGATGCTGTTTTGGCAGCCTGGGGGCC 569

QY 301 TGGGGAACAACATCTATCAGCACAGTTCAATTTTTTCCCTGAAAACCCCTGCGTTCTCAG 360
DB 570 TGGGGAACAACATCTATYAGCACAGTTCAATTTTTTCCCTGATAACCCCTGCGTTCTCAG 629

QY 361 CATGGGGGACAAAGTGGTCTCAAGGTGAGGACCCAGAGCTCAGCCTCTCCAGCA 417
DB 630 CATGGGGGACAAAGTGGTCTCAAGGTGAGGACCCAGAGCTCAGCCTCTCCAGCA 686

RESULT 29
BB068522
LOCUS
DEFINITION BB068522 RIKEN full-length enriched, 15 days embryo male testis Mus musculus cDNA clone 8030473016.3, similar to AK000398 Homo sapiens cDNA FLJ20391 f18, clone KAI4640, mRNA sequence.
ACCESSION BB068522
VERSION BB068522.2 GI:15404252
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 441)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps@mail.nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:
 NCI-CGAP clone distribution information can be found through the
 I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES source

Location/Qualifiers

1..441
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2713371"
 /clone_lib="NCI CGAP Sub3"
 /lab_host="DH10B (Life Technologies)"
 /notes="Vector: p7T3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The
 NCI CGAP Sub3 library is a subtracted library derived from
 the NCI CGAP Sub1 library, which is a subtracted library
 derived from B1. B1 constitutes a mixture of 21
 normalized or subtracted NCI CGAP libraries: NCI CGAP_Co4
 , NCI CGAP_P22, NCI CGAP_P28, NCI CGAP_Co10,
 NCI CGAP_Co16, NCI CGAP_P45, NCI CGAP_Kid12,
 NCI CGAP_Kid5, NCI CGAP_Kid11, NCI CGAP_Lym2,
 NCI CGAP_Br2, NCI CGAP_Co8, NCI CGAP_CLL1, NCI CGAP_Le12,
 NCI CGAP_Brn23, NCI CGAP_Lu5, NCI CGAP_Lu24,
 NCI CGAP_Lu19, NCI CGAP_GC4, NCI CGAP_GG6,
 NCI CGAP_Brn25. These 21 libraries were pooled and a
 single-stranded DNA preparation of the resulting mixture
 was used as a tracer in a subtractive hybridization with
 a driver whose composition is detailed below:
 NCI CGAP Kid3 pool 1 LLAM 3334-3337, 3682-3683,
 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775
 , 1500552-1502855); NCI CGAP Kid5 pool 1 LLAM 3338-3342
 , 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831,
 1471368-1472903, 1492104-1493255); NCI CGAP_Lu5 pool 1
 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991,
 1520904-1522439); NCI CGAP GC4 pool 1 LLAM 3164-3167,
 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,
 1469064-1470983, 1475592-1476743); NCI CGAP_P22 pool 1
 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs
 985608-986759, 1101192-1101959, 1217928-1220615);
 NCI CGAP_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE
 CloneIDs 1057416-1061255, 1144584-1145351). Subtraction
 was performed as previously described [Bonaldo, Lennon &
 Soares (1996): Normalization and Subtraction: Two
 Approaches To Facilitate Gene Discovery. Genome Research
 6, 791-806.
 TAG_LIB=NCI CGAP_Lu5
 TAG_TISSUE=Lung_
 TAG_SEQ=CAAC"

BASE COUNT 117 a 93 g 131 t
 ORIGIN

Query Match 19.6%; Score 397.6; DB 2; Length 441;
 Best Local Similarity 98.8%; Pred. No. 1.3e-90;
 Matches 411; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 979 GAGAAATACCAACACCGGTACAAATCCCGGACACCCAGGAGTGCCTTAGAA 1038
 Db

441 GAGAAATACCAACACCGGTACAAATCCCGGACACCCAGGAGTGCCTTAGAA 382

QY 1039 AAAGCCAAAGCAAGTGTGAAATATCAGTTTCTTACAGCACACCACTCCATCTTCGAC 1098

Db 381 AAAGCCAAAGCAAGTGTGAAATATCAGTTTCTTACAGCACACCACTCCATCTTCGAC 322

QY 1099 GACTTTGCTCACTACGAGAGCGCCA-GAGAGAGAGAGGTGGTGCAGAAAGCGCAG 1157
 Db 321 GACTTTGCTCACTACGAGAGCGCCAAGGAGGAGGTGGTGCAGAAAGCGCAG 262
 QY 1158 AGTCGAACCAACCAATGAGGCGGACCAAGTTCTTACATGTTCTAAAGTTTGACTTTGAA 1217
 Db 261 CGTCGAACCAACCAATGAGGCGGACCAAGTTCTTACATGTTCTAAAGTTTGACTTTGAA 202
 QY 1218 AACAGTTTAAACACAGTGTGCTTGGTCAGTCCAGTGTGTCGCCCGCGGGGTTGAG 1277
 Db 201 AACAGTTTAAACACAGTGTGCTTGGTCAGTCCAGTGTGTCGCCCGCGGGGTTGAG 142
 QY 1278 TGTGCACTTTGCTTTCTTGTGCTTGTGATTTTGGCCAGATGATCTGATTTATTTGT 1337
 Db 141 TGTGCACTTTGCTTTCTTGTGCTTGTGATTTTGGCCAGATGATCTGATTTATTTGT 82
 QY 1338 ACTTTTCTATGATTATTAATCTGTAGAAGTCACTAATAAGAGTATTTTTTTT 1393
 Db 81 ACTTTTCTATGATTATTAATCTGTAGAAGTCACTAATAAGAGTATTTTTTTT 26

RESULT 31

AL526609 826 bp mRNA linear EST 13-FEB-2001
 LOCUS AL526609 LTI_NFL003_NBC3 Homo sapiens cDNA clone CSODC020Y104 5
 DEFINITION prime, mRNA sequence.

ACCESSION AL526609.1 GI:12790102

VERSION EST.

KEYWORDS human.

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 826)

AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1..826

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CSODC020Y104"

/clone_lib="LTI_NFL003_NBC3"

/sex="male"

/tissue_type="neuroblastoma cells"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed

by Life Technologies. Contact : Feng Liang Life

Technologies, a division of Invitrogen 9800 Medical Center

Drive Rockville, Maryland 20850, USA Fax : (1) 301 610

8371 Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com>

BASE COUNT 168 a 270 c 239 g 147 t

ORIGIN 2 others

Query Match 19.5%; Score 396.4; DB 1; Length 826;

Best Local Similarity 98.3%; Pred. No. 3e-90;

Matches 411; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 CAAAGGACAAGATAATAAGTACAAAATGGTTTCGTTATCATCAGAAGGATACAGTTTCATG 60

Db 270 CAAAGGACAAGATAATAAGTACAAAATGGTTTCGTTATCATCAGAAGGATACAGTTTCATG 329

QY 61 CAATGACTTTGAGCCCTTACCTTACTGGACAGTCAAAATCAGAGTAAACAGTTACCCCTCAA 120

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Db 330 ACAATGACTTTGAGCCCTACCTTACTGAGCAGTCAAAATCAGAGTAAACAGTTTACCCCTCAA 389
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Qy 121 TGAGCCAGCCCTACCTGTCAGCTATTACCCGCGTCCATTTGGATTTCCTTACTCCCTCA 180
|||
Db 390 TGAGCCAGCCCTACCTGTCAGCTATTACCCGCGTCCATTTGGATTTCCTTACTCCCTCA 449
|||
Qy 181 ATGAGGCTCGGTGTTACTGAGGGGAGCCCTCCGATTCCATACCTCAGACCTACGGAC 240
|||
Db 450 ATGAGGCTCGGTGTTACTGAGGGGAGCCCTCCGATTCCATACCTCAGACCTACGGAC 509
|||
Qy 241 AGCTCAGTAACGGAGACCATCATTTTATGCAGATGCTGTTTGGGCGAGCTTGGGGCC 300
|||
Db 510 AGCTCAGTAACGGAGACCATCATTTTATGCAGATGCTGTTTGGGCGAGCTTGGGGCC 569
|||
Qy 301 TGGGGAACAACAT-CTATCAGCACAGTTCATTTTTCCTCGAAACCTCGGTTCTCA 359
|||
Db 570 TGGGGAACAACATCTATCAGCACAGTTCATTTTTCCTCGAAACCTCGGTTCTCA 629
|||
Qy 360 GCATGGGGGACAAGTGGGTCTCAAGTCTCAGCAGCCAGAGCTCAGCCTCTCCAGCA 417
|||
Db 630 GCATGGGGGACAAGTGGGTCTCAAGTCTCAGCAGCCAGAGCTCAGCCTCTCCAGCA 687
|||

RESULT 32
AL656188 702 bp mRNA linear EST 13-DEC-2001
LOCUS AL656188 XGC-neurula Silurana tropicalis cDNA clone TNeu035107 5',
DEFINITION mRNA sequence.
ACCESSION AL656188
VERSION AL656188.1 GI:17668416
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 702)
Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
TROPICALIS_SEQUENCE_ID: TNeu035107.sp6
Sequencing primer: Sp6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
FEATURES
Location/Qualifiers
1..702
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu035107"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from Sug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT 162 a 254 c 185 g 100 t 1 others
ORIGIN
Query Match 19.3%; Score 390.6; DB 1; Length 702;
Best Local Similarity 80.9%; Pred. No. 8.7e-89;
Matches 469; Conservative 0; Mismatches 105; Indels 6; Gaps 1;

Qy 436 CACCCGAGTATCAGAGCCCTCAGCAGCCACCCAGCCGCTGGGTGGCCCAACGCAC 495
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Db 129 CCACCCGCCCTCAGCAGCAGCCACAGCCCTCAGAACCCGCTGGGTGGCCCAACGCAC 188
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```

```

Qy 496 AGAAACGGCGCTTTGGGCAGAGCGGAGGGGTGGCAGGGATAGCAACTCTCTCTGAAAC 555
|||
Db 189 AGGAAACGGCTGTCTACCGCCAGGGCGGAGCGCCGAGC-----GGAAACCTCTGGCGGG 242
|||
Qy 556 GTCCAGCCTAATTTGCCCCCAGCGTCCAAATCCCAACCCGCTCTTTGAAAAAAGCTGAAGGCT 615
|||
Db 243 GCTCAGTCTCTCTCGCCCCCTGGGAACAGTCCCAACCCGCTCTGGAGNAAGCTGAAGGCC 302
|||
Qy 616 GCTCAGCTACAACCCGAAAGAGTTTGGTGGAAATCTGAAAGCGGGCGTGTGTTCAATC 675
|||
Db 303 GCCCAGCTACAACCCCAAGGACTTTGACTGGAACCTGAAAAACGGGCGCTGTTTCATA 362
|||
Qy 676 ATCAAGAGTCTCTGAGSAGACATCCACCGCTCATTAAGTACTCCATCTGGTGTAGC 735
|||
Db 363 ATAAAGAGTCTCTCGAGGAGACATCCACCGCTCATCAAGTACTCCATCTGGTGTAGC 422
|||
Qy 736 ACAGAGCAGCGCAACAGCGCTGCAGAGCGCTTCCGCTGCATGAGCAGCAAGGGGCC 795
|||
Db 423 ACAGAGCAGCGCAACAGCGCTGCATGAGGCTTCCGCTGCATGAAACGGCAAGGGGCC 482
|||
Qy 796 GTCTACCTCTCTTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCCGAGATGAAG 855
|||
Db 483 GTCTACCTCTCTTTCAGCGTCAACGGCAGCGACACTTCTCGCGCTGGCCGAGATGAAG 542
|||
Qy 856 TCCCGCTGGACTACGGCACAGTCCCGGGGTCTGGTCTCAGGACAAAGTGGAAAGGGGAAG 915
|||
Db 543 TCCCGCTGGACTACGGCACAGTCCCGGGGTCTGGTCTCAGGACAAAGTGGAAAGGGCAAG 602
|||
Qy 916 TTTGATGTCCTCAGTGGATTTTGTAAAGATGTACCAATACCAAGTCCCGCAGCATCAGG 975
|||
Db 603 TTCGAGCTCAAGTGGCTCTTCTGTCNAAGAGCTTCCCAACAGCAGCTGAGGCACATCCGC 662
|||
Qy 976 CTGGAATAACGACAAACAAACCGGTCAAAACTCCCGGG 1015
|||
Db 663 CTGGAATAACGACAAACAAACCGGTCAAAACTCCCGGG 702
|||

RESULT 33
AL524373 820 bp mRNA linear EST 13-FEB-2001
LOCUS AL524373 LTI_NFL003 NBC3 Homo sapiens cDNA clone CS0DC006Y03 5
DEFINITION prime, mRNA sequence.
ACCESSION AL524373
VERSION AL524373.1 GI:12787866
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 820)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequenage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..820
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC006Y03"
/dev_stage="neurula"
/lab_host="neuroblastoma cells"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center

```

Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 152 a 242 c 242 g 153 t 31 others
ORIGIN

Query Match 19.3%; Score 390.6; DB 1; Length 820;
Best Local Similarity 92.3%; Pred. No. 9.1e-89;
Matches 395; Conservative 21; Mismatches 11; Indels 0; Gaps 0;

```
QY 1 CAAAGGACAAGATATAAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 275 CAAAGGRCAGATATATWWTGTCAAWATGGTTCGTACATCAGAGGATACAGTTTCATG 334
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGATTAACAGTTACCCCTCAA 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 335 ACAATGAYTTTGAGCBCTACTCTTWTGCGGAGTAAATYAGAGTTACAGTTACCTCAA 394
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 TGAGCGACCCCTACCTGTCAGCTATTACCGCGCTCATTTGGATTTCCTTACTCCCTCA 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 395 TGAGCGACCCCTACCTGTCAGCTATTACCGCGCTCATTTGGATTTCCTTACTCCCTCA 454
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 ATGAGGCTCGGTGTTACTGACGGGACCTCCGATTCATACCTCACCCTACCGGAC 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 455 ATGAGGCTCGGTGTTACTGACGGGACCTCCGATTCATACCTCACCCTACCGGAC 514
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 AGCTCAGTACGGAGACCATCATTTATGACAGTGTGTTTTGGGACGCTGGGGGCC 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 515 AGCTCAGTACGGAGACCATCATTTATGACAGTGTGTTTTGGGACGCTGGGGGCC 574
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 301 TGGGGAACAACATCTATCAGCACAGGTTCAATTTTCCCTGAAACCCCTGCGTTCTCAG 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 575 TGGGGAACAACATCTATCAGCACAGGTTCAATTTTCCCTGAAACCCCTGCGTTCTCAG 634
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 361 CATGGGGACAAGTGGGTCTCAAGGTCAGAGCCAGAGCTCAGCTCTCCAGCA 417
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 635 CATGGGGACAAGTGGGTCTCAAGGTCAGAGCCAGAGCTCCGCGTATGGGAGCA 691
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 34
AL558224
LOCUS
DEFINITION AL558224 LTI_NFL008_Tc2 Homo sapiens cDNA clone CS0DJ001YF07 5
prime, mRNA sequence.

ACCESSION AL558224
VERSION AL558224.1 GI:12902542
KEYWORDS EST.

SOURCE
human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 773)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

JOURNAL

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1. .773

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DJ001YF07"

/clone_lib="LTI_NFL008_Tc2"

/sex="male"

/tissue types="T cells from T cell leukemia"

/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 154 a 260 c 219 g 139 t 1 others
ORIGIN

Query Match 19.0%; Score 385.4; DB 1; Length 773;
Best Local Similarity 98.1%; Pred. No. 1.9e-87;
Matches 411; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

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QY 1 CAAAGGACAAGATATAAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 277 CAAAGGACAAGATATAAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 336
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGATTAACAGTTACCCCTCAA 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 337 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGATTAACAGTTACCCCTCAA 396
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 TGAGCGACCCCTACCTGTCAGCTATTACCGCGCTCATTTGGATTTCCTTACTCCCTCA 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 397 TGAGCGACCCCTACCTGTCAGCTATTACCGCGCTCATTTGGATTTCCTTACTCCCTCA 456
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 ATGAGGCTCGGTGTTACTGACGGGACCTCCGATTCATACCTCACCCTACCGGAC 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 457 ATGAGGCTCGGTGTTACTGACGGGACCTCCGATTCATACCTCACCCTACCGGAC 516
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 240 CAGCTCAGTAACGGAGACCATCATTTTATGACAGTGTGTTTTGGGACGCTGGGGGCC 299
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 517 CAGCTCAGTAACGGAGACCATCATTTTATGACAGTGTGTTTTGGGACGCTGGGGGCC 576
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 300 CTGGGGACAACAATCTATCAGCACAGGTTCAATTTTCCCTGAAACCCCTGCGTTCTCA 359
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 577 CTGGGGACAACAATCTATCAGCACAGGTTCAATTTTCCCTGAAACCCCTGCGTTCTCA 636
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 360 GCAT-GGGGGACAAGTGGGTCTCAAGGTCAGAGCCAGAGCTCAGCTCTCCAGCA 417
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 637 GCATGGGGGACAAGTGGGTCTCAAGGTCAGAGCCAGAGCTCCGCGTATGGGAGCA 695
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 35
AL580105/c

LOCUS

DEFINITION AL580105 LTI_NFL008_Tc2 Homo sapiens cDNA clone CS0DJ001YF07 3

prime, mRNA sequence.

ACCESSION AL580105

VERSION AL580105.1 GI:12945803

KEYWORDS EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 772)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

JOURNAL

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1. .772

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DJ001YF07"

/clone_lib="LTI_NFL008_Tc2"

/sex="male"

/tissue type="T cells from T cell leukemia"

/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com>

BASE COUNT 275 a 168 c 148 g 176 t 5 others
ORIGIN

Query Match 19.0%; Score 384.4; DB 1; Length 772;
Best Local Similarity 98.3%; Pred. No. 3.4e-87;
Matches 395; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

QY 1627 TTTTGTTCATCTGCTGATTTTATTAATCTGTTATCGTCTAAAGTGTAAATTAC 1686
Db TTTTGTTCATCTGCTGATTTTATTAATCTGTTATCGTCTAAAGTGTAAATTAC 713

QY 1687 CAAATTTGATTTTCTGTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTT 1746
Db CAAATTTGATTTTCTGTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTT 653

QY 1747 TTTTGTTCATCTGCTGATTTTATTAATCTGTTATCGTCTAAAGTGTAAATTAC 1806
Db TTTTGTTCATCTGCTGATTTTATTAATCTGTTATCGTCTAAAGTGTAAATTAC 595

QY 1807 TCATGTCCTGCTGCTGATTTTATTAATCTGTTATCGTCTAAAGTGTAAATTAC 1866
Db TCATGTCCTGCTGCTGATTTTATTAATCTGTTATCGTCTAAAGTGTAAATTAC 535

QY 1867 GAAGTGCTTTAGTCTGCTGATTTTATTAATCTGTTATCGTCTAAAGTGTAAATTAC 1926
Db GAAGTGCTTTAGTCTGCTGATTTTATTAATCTGTTATCGTCTAAAGTGTAAATTAC 475

QY 1927 ATTTTACACTTTTCTTAAAGATTTCTAATGCGCTCTTAAGTCTTTTATACCAATATGCTG 1986
Db ATTTTACACTTTTCTTAAAGATTTCTAATGCGCTCTTAAGTCTTTTATACCAATATGCTG 415

QY 1987 AGCTTTAAGTGTAGGATCTGTTAGTGTACAGACAGTGTGATGGA 2028
Db AGCTTTAAGTGTAGGATCTGTTAGTGTACAGACAGTGTGATGGA 373

RESULT 36
AW766504/c
LOCUS
DEFINITION
IMAGE:3195605 3' similar to TR:064526 064526 YUP8H12R.13 PROTEIN.
; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW766504
AW766504.1 GI:7698494
EST.
Xenopus laevis
African clawed frog.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.

REFERENCE
AUTHORS

Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person,
B., Gibbons, M., Harvey, N., Ritter, E., Jackson, J., McCann, R.,
Waterston, R. and Wilson, R.
WashU Xenopus EST project, 1999
Unpublished (1999)

TITLE
JOURNAL
COMMENT

Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by R. Harland, PhD. (University of California,
Berkeley)
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LUNL at:
image.llnl.gov/image/html/iresources.shtml
Seg primer: -40UP from Gibco
High quality sequence stop: 503.
Location/Qualifiers
source
1. .659
/organism="Xenopus laevis"
/db xref="taxon:8355"
/clone="IMAGE:3195605"
/clone_lib="Harland stage 19-23"
/tissue_type="neurula"
/dev_stage="stage 19-23"
/lab_host="DH10B (phage-resistant)"
/note="Vector: pCS107 (custom); Site 1: NotI; Site 2: SalI
; cDNA made by oligo-dT priming. Library constructed by
Dr. Francesca Mariani in the laboratory of R. Harland,
Ph.D. (University of California, Berkeley). References:
XBP-2 is a transcriptional repressor that converts
ectoderm into neural tissue. Mariani, F.V. Harland, R.M.,
Development. 1998 Dec;125(24):5019-31. PMID: 9811586; UI:
99030283; Use of large-scale expression cloning screens in
the xenopus laevis tadpole to identify gene function.
Grammer TC, Liu KJ, Mariani FV, Harland RM, Dev Biol.
2000 Dec 15;228(2):197-210. PMID: 11112324; UI: 20564075;
Note: This is a Xenopus Gene Collection (XGC) library."

BASE COUNT 148 a 161 c 153 g 196 t 1 others
ORIGIN

Query Match 17.9%; Score 363; DB 2; Length 659;
Best Local Similarity 82.5%; Pred. No. 9e-82;
Matches 439; Conservative 0; Mismatches 91; Indels 2; Gaps 2;

QY 625 TACAACCCGAAGAGTGTGAGTGGAAATCTGAAAAGCGGCGTGTCTATCATCAAGAGC 684
Db TATAACCCCTAGGATTTTGTAGTGGAACTTGAATAATGACGTGTGTATATAAGAGT 600

QY 685 TACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCCATCTGCTGTAGCAGAGCAC 744
Db TATT-TGAGGATGATATCCCGNGTTCCATCATATTCATTTGGTGACGACAGAGCAT 541

QY 745 GGCACAAAGCGCTGACAGCGCTTCGCTGCATGAGGACAAAGGGCCGCTTACCTG 804
Db GGGAAATAACCGTTGGATAACGCTTTCGCTCCATGAATGGCAAGGGCCGCTTACCTT 481

QY 805 CTCTTCAGCGCTCAATGGGAGTGGGCAATTTTGTGGGGTGGCGAGATGAAGTCCCGCGT 864
Db CTGTTTCAGCGCTCAACGGCAGTGGACACTTTTTCGGCGGTAGCCGAGATGAAGTCCCGCGT 421

QY 865 GACTACGGCACCAGTCCCGGGGTCTGGTCTCAGGACAAAGTGAAGGGGAAGTTGATGTC 924
Db GACTATGGCACCAGTCCCGGTCTGTGTGTGTCACAGGACAAATGCAAGGGCAAGTTTGCAGTC 361

QY 925 CAGTGGATTTTGTAAAGATGTACCCAAATACAGCTCCGCGACATCAGGCTGGAGAAAT 984
Db AAGTGGCTCTTTGTCAAGAGACGTTCCCAACACAGCTGAGGCACATCCGCTGGAGAAAT 301

QY 985 AACGACACAAACCGGTCAAACTCCCGGGACACCCAGAGGTGCTCTTACAAAAGCC 1044
Db AACGACACAAACCGGTCAAACTCCCGGGACACCCAGAGGTGCTCTTACAAAAGCA 241

QY 1045 AAGCAAGTGTCTGAAAATTTATCAGTTCTCTACAGGACACAACTCCATCTTCGACGACTTT 1104
Db AACTGTGTCTTAATTAATCATTGCCACTTACAGGACACAGACCTCCATCTTTGATGACTTT 181

QY 1105 GTCTACTACGAGAACGCCCA-CAGGAGGAGGAGGTGGTGGCGCAAGAACGGC 1155
Db TCTCATTACGAGAACGCCGAGGAGGAGGAGGTGGTGGCGCAAGTAACGC 129

RESULT 37
BS542677
LOCUS
BE542677 790 bp mRNA linear EST 09-AUG-2000

RESULT 38

GAGAGAGAGCGCGCGCACTCGAGTTTTTTTTTTTTTTTTTTN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5',
GAGAGAGATTCGAGTTTAATTAATATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI." 1 others
BASE COUNT 218 a 292 c 276 g 223 t

Query Match 17.0%; Score 345; DB 2; Length 1010;
Best Local Similarity 89.2%; Pred. No. 3.9e-77;
Matches 372; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CAAAGGCAAGATAAAGTACAAATGGTTCGTATACAGAGGATACAGTTTCATG 60
Db 237 CAAAGGCAAGATAAAGTACAAATGGTTCGTATACAGAGGATACAGTTTCATG 296
Qy 61 ACAATGACTTTGAGCCCTACCTTACTGACAGTCAAAATCAGAGTACAGTTACCCCTCAA 120
Db 297 ACAATGACTTTGAGCCCTACCTTCTGGACAGTCCAAATCCGAGTAAACAGTTACCCCTCGA 356
Qy 121 TGAGGAGCCCTACCTGTCAGTATTACCGCGCTGCAATTCGATTCCTTACTCCCTCA 180
Db 357 TGAGTATCCCTTACCTGTCAGTATTACCGCGCTGCAATTCGATTCCTTACTCCCTCA 416
Qy 181 ATGAGGCTCCGTGCTACTGAGGGGACCTCCGATTCATACCTCAGCAGTACGGAC 240
Db 417 GCGAGGACCATGGTCCACTGACGGGACCTCCGATTCATACCTCAGCAGTACGGAC 476
Qy 241 AGCTCAGTTAAGGAGACCATCATTTTATGACAGTCTGTTTTGGGAGCCTGCGGGCC 300
Db 477 AACTTAGTAATGAGACCATCACTTCATGATGATGCTTTTTGGGAGCCTGCGGGTC 536
Qy 301 TGGGAGACACATCTATGACAGCAGTTCAATTTTTTCCCTGAAACCTGCTTCAG 360
Db 537 TGGGAGACACATCTTACCAGCAGGTTTAATTTTTTCCCTGAAACCTGCAATTCAG 596
Qy 361 CATGGGGGCAAGTGGTCTCAAGGTGACAGACCCAGAGCTCAGGCTCTCCAGCA 417
Db 597 CATGGGGGCAAGTGGTCTCAGGGGACAGACTCAGAGCTCAGGCTATGGAGCA 653

RESULT 39
AL515909
LOCUS
DEFINITION ALS15909 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA001YB18 5
prime, mRNA sequence.
ACCESSION ALS15909
VERSION ALS15909.1 GI:12779402
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 917)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..917
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DA001YB18"
/clone_lib="LTI_NFL011_NBC1"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH108"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 174 a 274 c 228 g 206 t 35 others
ORIGIN
Query Match 16.7%; Score 338; DB 1; Length 917;
Best Local Similarity 88.8%; Pred. No. 2.3e-75;
Matches 366; Conservative 17; Mismatches 27; Indels 2; Gaps 2;
Qy 1 CAAAGGCAAGATAAAGTACAAATGGTTCGTATACAGAGGATACAGTTTCATG 60
Db 278 CAAAGGCAAGATAAATWTTTACAAATGGTTCGTATACATCATAGGWTATATTTCATT 337
Qy 61 ACAATGACTTTGAGCCCTACCTTACTGACAGTCAAAATCAGAGTAAACAGTTACCCCTCAA 120
Db 338 AYATATATTTTACCTTACTGACATTTAAATYAGATTTTACATTACCCCTYAA 397
Qy 121 TGAGGAGCCCTACCTGTCAGTATTACCGCGCTGCCATTGGATTTCTTACTCCCTCA 180
Db 398 TTAGTACCCCTACCTTTCAGTATTATGCGYTTTATTGGATTTCTTACTCCCTCA 457
Qy 181 ATGAGGCTCCGTG-GTCTACTGACGGGACCTCCGATTCATACCTCAGCAGTACCGA 239
Db 458 ATGAGGCTCCGTGTCATTTCTGGTACCTCCGATTCATACCTCAGCAGTACCGA 517
Qy 240 CAGCTCAGTAAAGGAGACCATCATTTTATGACAGTATGCTTTTTGGGAGCCTCGGGGC 299
Db 518 CAGCTCAGTAAAGGAGACCATCATTTTATGACAGTATGCTTTTTGGGAGCCTCGGGGC 577
Qy 300 CTGGGGAACAACATCTATCAGCAGAGTTCAATTTTTTCCCTGAAAAACCTCGCTTCCTCA 359
Db 578 CTGGGGAACAACATCTATCAGCAGAGTTCAATTTTTTCCCTGAAAAACCTCGCTTCCTCA 637
Qy 360 GCAT-GGGGGACAGTGGTCTCAAGGTGACGAGACCCAGAGCTCAGGCTCTCT 410
Db 638 GCATGGGGGACAGTGGTCTCAAGGTGACGAGACCCAGAGCTCCGGGTAT 689

RESULT 40
AA460050
LOCUS
DEFINITION AA460050 355 bp mRNA linear EST 09-JUN-1997
IMAGE:796418 5' similar to TR:G849195 G849195 CHROMOSOME IV COSMID 9481.; mRNA sequence.

ACCESSION AA460050
VERSION AA460050.1 GI:2184934
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 355)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.

TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LLNL; contact the

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

FEATURES

source

1. 341
/organism="Homo sapiens"
/db_xref="ATCC (inhost):165217"
/db_xref="taxon:9606"
/clone_lib="T-cell lymphoma"
/cell_type="T-lymphocyte"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 91 a 80 c 86 g 82 t 2 others
ORIGIN

Query Match 16.1%; Score 327; DB 1; Length 341;
Best Local Similarity 99.1%; Pred. No. 1.1e-72;
Matches 338; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 991 AACAAACGGGTCAAACTCCGGGACACCCAGGAGTGCCCTTAGAAAAAGCCAAAGCAA 1050
Db 1 AACAAACGGGTCAAACTCCGGGACACCCAGGAGTGCCCTTAGAAAAAGCCAAAGCAA 60

QY 1051 GTGCTGAAATATACGTTCTTACAGCACACACCTCCATCTTCGACGACTTTGCTCAC 1110
Db 61 GTNCTGAAATATACGTTCTTACAGCACACACCTCCATCTTCGACGACTTTGCTCAC 120

QY 1111 TACGAGAAGCGCCA-GAGGAGGAGGAGTGTCGCAAGCAACCGCAGAGTCGAAACAAA 1169
Db 121 TACGAGAAGCGCCAGGAGGAGGAGTGTCGCAAGCAACCGCAGAGTCGAAACAAA 180

QY 1170 CAATGAGGGGGAACAGTTCTTACATGTTCTAACGTTTGAATTTGAAACAGTTTAAAA 1229
Db 181 CAATGAGGGGGAACAGTTCTTACATGTTCTAACGTTTGAATTTGAAACAGTTTAAAA 240

QY 1230 CACGTGCTTGTGTCAGTCAGTGTCGTCGCGTCGCGGGTTGAGTTGTCATCTTT 1289
Db 241 CACGTGCTTGTGTCAGTCAGTGTCGTCGCGCGGGTTGAGTTGTCATCTTT 300

QY 1290 GCCTTTCTTGTGTTGATTTTGTCCAGATGGATCTGCATT 1330
Db 301 GCCTTTCTTGTGTTGATTTTGTCCAGATGGATCTGCATT 341

RESULT 44
AW465429
LOCUS
DEFINITION AW465429 530 bp mRNA linear EST 24-FEB-2000
clone BP230019A20A9 Soares normalized bovine placenta Bos taurus CDNA

ACCESSION AW465429
VERSION AW465429.1 GI:7035597
KEYWORDS EST.
SOURCE cow.

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovine; Bos.
REFERENCE 1 (bases 1 to 530)
AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinaz,J., Liu,L. and Larson J.H.

TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi 9:

Cross match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
PCR Primers

FORWARD: TAATACGACTCACTATAGG

BACKWARD: ATTAACCTCACTAAG

Insert Length: 530 Std Error: 0.00

Plate: BP230019A20 row: A column: 9

Seq primer: AGCGATAACAATTTCCACACAGA

High quality sequence stop: 530.

Location/Qualifiers

FEATURES

source

1. 530

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone="BP230019A20A9"

/lab_host="Soares normalized bovine placenta"

/sex="female"

/lab_host="DH10B"

/notes="Organ: placenta; Vector: p773Pac; Site_1: EcoRI;

Site_2: NotI; The cDNA library was contributed by the

Soares laboratory and it was constructed and normalized

as described by Bonaldo, M.F., Lennon, G. and Soares,

M.B. (1996), Genome Research 6(9): 791-806."

BASE COUNT 154 a 122 c 126 g 128 t

ORIGIN

Query Match 16.1%; Score 326.8; DB 2; Length 530;

Best Local Similarity 76.0%; Pred. No: 1.4e-72;

Matches 403; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 594 CGTCTTGAATAACTGAGGCTGCTCACAGCTACACCCGAAAGAGTTTCAGTGGATCT 653

Db 1 CGTCTTGGAGAAGTTTCGGTCCATTAATACTATACCCCAAGGATTTTCACTGGATCT 60

QY 654 GAAAGCGGCGGTGTTCATCATCAAGAGTACTCTGAGGAGACATCCACCGCTCCAT 713

Db 61 GAACATGCGCGGTTTCATCATTAAGAGTACTCGAGGAGATATCCACGTTCCAT 120

QY 714 TAAGTACTCATCTGTTAGCAGACGACGCAACAGCGCTCGACAGCGCTTCCG 773

Db 121 TAAGTATAATCTGTTGACGACAGAGCATGGTAACAGAGACTGGATCTGCTTATCG 180

QY 774 CTGATGACGACGCAAGGGGCGCTCTACCTGCTTTCAGCGTCAATGGGAGTGGCATTT 833

Db 181 CTCATGAACGGAAAGGCGGCTTACTTACTTTTTCAGTGTCAACGGCAGTGGACATT 240

QY 834 TTGTGGGTCGCGAGATGAAGTCCCGTGGACTACGGCAGCTGCGGGGTCTGGTC 893

Db 241 CTGTGTGTCGAGAATGAAATCTGCTGGACTACACACATGTGCAGGTGTGGTC 300

QY 894 TCAGGACAAGTGGAAAGGGGAAAGTTTGTATGCCAGTGGATTTTGTAAAGGATGTACCAA 953

Db 301 CCAGGACAAATGGAAGGGCGGTTTGTATGTCAGGTGGATTTTGTGAAGGACGTTCCAA 360

QY 954 TAACGAGTCCGACACATCAGGCTGGAGATACGACAAACCCGTCACAACTCCG 1013

Db 361 TAGCCAACTCGACACATTCGCTAGAGAAACAGAGATAAACAGTACCACTCCAG 420

QY 1014 GGACACCCAGAGTGCCTTTAGAAAAGCAAGCAAGTGTCTGAAAATATCAGTTCTTA 1073

Db 421 GGACACTCAGGAAGTGCCTCTGAAAAGCTAAGCAGGTGTTGAAAATCATACCCAGCTA 480

QY 1074 CAAGCACACAACTCCATCTTCGACGACTTTGTCTACTACGAGAAGCGCC 1123

Db 481 CAAGCACCACTTCCATTTTTCATGACTTCTCACACTATGAGAAAGCGCC 530

RESULT 45

AL774891

LOCUS

DEFINITION AL774891 XGC-gastrula Silurana tropicalis cDNA clone TGae080113 5',

mrna sequence.

ACCESSION AL774891

VERSION AL774891.1 GI:21560595

AL774891 654 bp mRNA linear EST 25-JUN-2002

AL774891 XGC-gastrula Silurana tropicalis cDNA clone TGae080113 5',

mrna sequence.

AL774891 GI:21560595

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

EST.
western clawed frog.
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Silurana.
Taylor, R., Ashurst, J.L., Croning, M.D.R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2002
Unpublished (2001)
Contact: Taylor R
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
TROPICALIS_SEQUENCE_ID: TGAS080113.plkSP6
Sequencing primer: FikSP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
1. 654
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TGAS080113"
/clone_lib="XGC-gastrula"
/lab_host="Escherichia coli XLI-blue"
/notes="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dt primed from Sug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."

BASE COUNT      152 a  229 c  175 g   98 t
ORIGIN
Query Match      15.9%; Score 322.4; DB 1; Length 654;
Best Local Similarity 80.9%; Pred. No. 2e-71;
Matches 390; Conservative 0; Mismatches 86; Indels 6; Gaps 1;

QY 436  CACCCGACGTATCAGAGCCCTCAGCAGCCACCCGCGCTGGTGTCCCGCCACGCAAC 495
DB 179  CCACGCCCCCTCAGCAGCAGCCACGAGGCCCTTCAGAACCGCTGGTGGCCCCCAGCAAC 238
QY 496  AGAAACCGCGCTTTGGGAGAGCGGAGGGCTGGCAGCGATAGCAACTCTCTGGAAAC 555
DB 239  AGGAACGCTGCTTACGCGCAGGCGGA-----GGCCCGGACGGAACTCTTGGGCGG 292
QY 556  GTCCAGCCCTAATTTCTGCCCCCAGCGTTCGAATCCACCCCGTCTTGGAAACCTGAAGGCT 615
DB 293  GCTCAGTCTCACTCCGCCCCCTGGGAACGAGTCCACCCCGTCTGGAGAACTGAAGGCC 352
QY 616  GCTCAGCTTACAAACCGGAAGATTGTAGTGAATCTGAAGCGGGCTGTGTTTCATC 675
DB 353  GCCACAGCTACAAACCCCAAGGACTTTGACTGGAACTTGAAGAACTGAAACCGGGCGGTTCATA 412
QY 676  ATCAAGAGTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCCATCTGGTGTAGC 735
DB 413  ATAAAGAGTACTCCGAGGACGACATCCACCGCTCCATCAAGTACTCCATCTGGTGCAGC 472
QY 736  ACAGAGCAGCGCAACAAAGCGCTTGGACAGCGCTTTCGCTGCATGAGCAAGAGGGCCCC 795
DB 473  ACAGAGCAGCGCAACAAAGCGCTTGGACAGCGCTTTCGCTGCATGAAACGCAAGGGCCCC 532
QY 796  GTTACTCTGCTCTCAGCGTCAATGGAGTGGGCAATTTTGGGGTGGCCGAGATGAAG 855
DB 533  GTTACTCTTCTGTTACGCGTCAACGCGCAGCGACACTTCTGCGGCGTGGCCGAGATGAAG 592
QY 856  TCCCGCTGACTACGCGACAGTGGCGGGCTCTGGTCTCAGGACCAAGTGGAAAGGGGAAG 915
DB 593  TC0000TGGACTACGCGACAGTGGCGGGCTCTGGTTCGCGAGCAAGTGGAAAGGGCAAG 652
QY 916  TT 917
||

```

us-09-877-633-2.rst

Db 653 TT 654

RESULT 46
AA377640
LOCUS
DEFINITION
EST90244 Synovial sarcoma Homo sapiens cDNA 5' end, mRNA sequence.
AA377640
VERSION
AA377640.1 GI:2029960
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 338)
AUTHORS
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult
C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White
O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,
Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,
Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,
Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,
Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,
Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon
M.R., Rosen, C.A., Haseitine, W.A., Fields, C., Fraser, C.M. and
Venter, J.C.

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
Other ESTs: THCI92215
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlavage@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse
Location/Qualifiers
1. 338
/organism="Homo sapiens"
/db_xref="ATCC (inhost):182015"
/db_xref="taxon:9606"
/clone_lib="Synovial sarcoma"
/sex="female"
/tissue type="synovial membrane"
/dev stage="adult, 20 yrs"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 102 a 51 c 49 g 136 t
ORIGIN
Query Match 15.8%; Score 320.6; DB 1; Length 338;
Best Local Similarity 98.5%; Pred. No. 4.7e-71;
Matches 334; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1372 CTAATAAAGAGGATTTTTTTTGTTCAGCTTATCAATCAGACTGATCTTAATGGAATGT 1431
DB 1 CTAATAAAGAGGAT-TTTTTTTGTTCAGCTTATCAATCAGACTGATCTTAATGGAATGT 59
QY 1432 AGTATCCTTAAACAAAGCATCTATTTTGGCAGAAATTTGTTCTTAAATTCAGTCAT 1491
DB 60 AAGTATCCTTAAACAAAGCATCTATTTTGGCAGAAATTTGTTCTTAAATTCAGTCAT 119

QY 1492 TTGATATTTCTGTGAGACTCATATTTCTCATCCCTTTATTTGCTTTTGTAGCAACATAGA 1551
Db 120 TTGATATTTCTGTGAGACTCATATTTCTCATCCCTTTATTTGCTTTTGTAGCAACATAGA 179
QY 1552 AACCATGAGTCATTTTGTCAATTTAGAGTATTTCTGATAAAATCTCTTGAAATACTGAAAT 1611
Db 180 AACCATGAGTCATTTTGTCAATTTAGAGTATTTCTGATAAAATCTCTTGAAATACTGAAAT 239
QY 1612 CAAAGGTTAATGATTTTGTCTCAATTTGATTTGTCATTTTATTTATCTGTTATCGGTC 1671
Db 240 CAAAGGTTAATGATTTTGTCTCAATTTGATTTGTCATTTTATTTATCTGTTATCGGTC 299
QY 1672 AAAGTCTAATTTACCATTTGATTTTCTGCTAGACAG 1710
Db 300 AAAGTCTAATTTACCATTTGATTTTCTGCTAGACAG 338

RESULT 47
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LOCUS
DEFINITION BP230019A20B7 Soares normalized bovine placenta Bos taurus cDNA
clone BP230019A20B7 5', mRNA sequence.
ACCESSION AW465438
VERSION AW465438.1 GI:7035606
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 521)

Lewin,H.A., Soares,M.B., Rebeiz,M., Pardini,J., Liu,L. and Larson
J.H.
Bovine ESTs
Unpublished (2000)
Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATACGACTCACTATAGG
BACKWARD: ATTAACCTCTCACTAAG
Insert Length: 521 Std Error: 0.00
Plate: BP230019A20 row: B column: 7
Seq primer: AGCGGATACATTTACACAGGA
High quality sequence stop: 521.
Location/Qualifiers
1. .521
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/db_xref="taxon:9913"
/clone="BP230019A20B7"
/sex="female"
/lab_host="DH10B"
/notes="Organ: placenta; Vector: pTT3Pac; Site 1: EcoRI;
Site 2: NotI; The cDNA library was constructed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."

BASE COUNT 150 a 119 c 124 g 128 t
ORIGIN

Query Match 15.7%; Score 319.4; DB 2; Length 521;
Best Local Similarity 75.8%; Pred. No. 1.1e-70;
Matches 395; Conservative 0; Mismatches 126; Indels 0; Gaps 0;
QY 594 CGTCTTTGAAAAACTGAAGGCTGTCTACAGCTACAAACCCGAAAGAGTTTGTAGTGGAAATCT 653
Db 1 CGTCTTTGAGAGAGCTTCGGTCCATTAACTATTAACCCAGGATTTTGTAGTGGAAATCT 60
QY 654 GAAAGCGGCGGTGTGTTCATCATCAAGAGCTACTCTGAGGACGACATCCACCGCTCCAT 713
Db 61 GAAACATGGCGGGGTTTTCATCATTAAGAGCTACTCCGAGGACGATATCCACCGTTCAT 120
QY 714 TAAGTACTCATCTGTGTAGCAGAGCAGCGCAACAGCGCTGAGCAGCGCTTCCG 773
Db 121 TAAGTATAATATCTGTGTGACAGCAGAGCATGGTAAACAGAGACTGGATGCTGTATCG 180
QY 774 CTGCATGAGCAGCAAGGGGCGGCTCTACCTGCTCTTCAGGGTCAATGGGAGTGGCATTT 833
Db 181 CTCATGAAAGGAGGAGGCGGCTTACTTTTCTGTTTCAACGGCAGTGGACACTT 240
QY 834 TTGTGGGTGGCCGAGATGAAGTCCCGCTGGACTACGGCAGCAGTCCCGGGTCTGGTC 893
Db 241 CTGTGGTGTGCGAGAAATGAAATCTGCTGTGGACTACACACATGTGCAGGTGTGGTC 300
QY 894 TCAGGACAAGTGGAGGGGAGTTTGTATGTCAGTGGATTTTGTAAAGATGTACCCAA 953
Db 301 CCAGGACAAATGGAAGGGGCGGTTTGTATGTCAGTGGATTTTGTGAAGCAGCTTCCAA 360
QY 954 TAACCACTCCGACACATGAGTGGAGATTAACGACAAACCCGCTCAAACTCCG 1013
Db 361 TAGCAACTCGACACATTCGCTTAGAAGAACAGAGATTAACCACTGACCACTCCAG 420
QY 1014 GGACACCCAGAGGTGCGCTTAGAAAAAGCAAGCAAGTGTGAAAAATTTATCAGTTCTTA 1073
Db 421 GGACACTCAGAGAGTGCCTCTCGAAAAAGCTAAGCAGGTGTTGAAAAATCATAGCCAGCTA 480
QY 1074 CAGACACAACTCCATCTTCGACGACTTTGCTCACTACG 1114
Db 481 CAAGCACCACCTTCCATTTTGTATGACTTCTCACACTATG 521

RESULT 48
AV711963
LOCUS
DEFINITION AV711963 DCA Homo sapiens cDNA clone DCAAABC07 5', mRNA sequence.
ACCESSION AV711963
VERSION AV711963.1 GI:10731269
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 383)
Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,
G., Cheng,Z. and Han,Z.
Homo sapiens cDNA DCA clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. .383
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DCAAABC07"
/clone_lib="DCA"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1. .780
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="BMFAWB05"
/clone_lib="BM"
/tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_hosts="BM25.8"
/notes="Vector: pTriplEx2; Site 1: sfIIA; Site 2: sfIIIB"
BASE COUNT 234 a 147 c 170 g 226 t 3 others
ORIGIN

Query Match 15.2%; Score 307.8; DB 2; Length 780;
Best Local Similarity 75.1%; Pred. No. 1.1e-67;
Matches 384; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 629 ACCGGAAGAGTTTGGTGGAACTCTGAAAGCGGCGTGTTCATCATCAAGAGCTACT 688
DB 72 ATCCCAAGACTTTGATTTGGAATCTGAGATGAGCGTGTGTTATATTTAAAGCTACT 131
QY 689 CTGAGGACGACATCCACCGTCTCAATTAAGTACTCCATCTGTGTGAGCAGACGCGCA 748
DB 132 CTGAGGATGACATACATCGTTTCCATTAATACTCTATCTGTGTGAGTACTGAGCATGTA 191
QY 749 ACAAGCCCTGGACAGCGCTTCCGCTGCATGACGACAGGGGCCGTCTACCTGCTCT 809
DB 192 ATAAGCGTTTGGATGCGACTTACCGTTCCCTGAAATGGGAAAGGCCCACTCTATTACTCT 251
QY 809 TCAGCGTCAATGGAGTGGGCAATTTTGTGGGCGCGAGATCAAGTCCCGCTGGACT 868
DB 252 TCAGTGTGAATGGCAGTGGACATTTTGTGGAGTGGCTGAAATGAAGTCTGTGTGGACT 311
QY 869 ACGSCACAGTCCCGGGTCTGTGCTCAGGACAAAGTGAAGGGGAAGTTTGTATGCCAGT 928
DB 312 ATAATGCGTATGCTGGTCTGTGCTCAGGATAAGTGGAGGGCAAAATTTGAAGTTAAAT 371
QY 929 GGATTTTGTAGGATGATCCCAATTAACCGCTCCGGCACATCAGGCTGGAGAAATACG 988
DB 372 GGATCTTTGTCAAGATGTTTCCCAATTAACCAATTAACGGCATATTTCGCTTAGAAAATAATG 431
QY 989 ACAACAAACCGGTCACAAATCCCGGACACCCAGGAGGTGCCCTTAGAAAAAGCCCAAGC 1048
DB 432 ACAACAAACCGGTTACCAATTCAGGGACACTCAAGAGGTACCCCTAGAAAAAGGCTAAGC 491
QY 1049 AAGTGCTGAAAATTTATCAGTTTCTTACAAGCACACAACCTCCATCTTCGACGACTTTGCTC 1108
DB 492 AAGTGCTTAAATAATTTGCTACTTTTCAAGCATACCACTCAATCTTTGATGACTTTGAC 551
QY 1109 ACTAGAGAGCGCCAGAGGAGGAGGAGTG 1139
DB 552 ATTATGCGCTCAAGAGAGGAGGAGGAGCCATG 582

RESULT 51
BE242919 326 bp mRNA linear EST 03-OCT-2001
LOCUS TCAAP1E2446 Pediatric acute myelogenous leukemia cell (FAB M1)
DEFINITION Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP2446, mRNA sequence.
ACCESSION BE242919
VERSION BE242919.1 GI:9094652
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 326)

AUTHORS Wei, Y., Tsang, Y. T. M., Mei, G., Ku, J. M., Ali-Osman Jr., F. R., Muzny, D., Bouck, J., Gibbs, R. A. and Margolin, J. F.
TITLE Pediatric Leukemia cDNA Sequencing Project
JOURNAL Unpublished (2000)
COMMENT Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@ccc.org
Citation: Carninci, P. and Hayashizaki, Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer.
Location/Qualifiers
1. .326
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TCAAP2446"
/clone_lib="Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA"
/sex="male"
/tissue_type="leukopheresis"
/cell_type="myeloid cell"
/dev_stage="pediatric 6 years"
/lab_host="DH10B"
/notes="Vector: lambda pSB; Site 1: BamHI; Site 2: EcoRI;
First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGACTCGAGCGCGCAGGAG(T)VN 3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand was primed with a BamHI-dC primer [5'AGAGCTCGATCCCGCCGCAATAATAAT(C) 3']. Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoaka S, Sasaki, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)."
BASE COUNT 75 a 97 c 77 g 77 t
ORIGIN

Query Match 15.1%; Score 307; DB 2; Length 326;
Best Local Similarity 96.9%; Pred. No. 1.3e-67;
Matches 313; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 95 AAATCAGAGTAAACAGTTACCCCTCAATGAGCGACCCCTACCTGTCAGCTATTACCGCC 154
DB 2 AAATCAGAGTAAACAGTTACCCCTCAATGAGCGACCCCTACCTGTCAGCTATTACCGCC 61
QY 155 GTCATTGGATTTTCCTTACTTCCCTCAATGAGGCTCGTGTCTACTGCGGGGACCCCTCC 214
DB 62 GTCATTGGATTTTCCTTACTTCCCTCAATGAGGCTCGTGTCTACTGCGGGGACCCCTCC 121
QY 215 GATTTCATACCTCACCACCTTACGAGCAGCTCAGTACGGAGACCATCTTTTATGACGA 274
DB 122 GATTTCATACCTCACCACCTTACGAGCAGCTCAGTACGGAGACCATCTTTTATGACGA 181
QY 275 TGTGTTTTTGGGACGCTGGGGCCTGGGGAAACAATCTATCAGACAGGTTCAATTT 334
DB 182 TGCTGTTTTTGGGACGCTGGGGCCTGGGGAAACAATCTATCAGACAGGTTCAATTT 241
QY 335 TTTTCCCTGAAAACCTTCCGCTTCTCAGCATGGGGGACAAAGTGGCTCTCAGGTCAGGAC 394
DB 242 TTTTCCCTGAAAACCTTCCGCTTCTCAGCATGGGGGACAAAGTGGCTCTCAGGTCAGGAC 301
QY 395 CCAGAGCTCAGCCTCTCCACGCA 417
DB 302 CCAGAGCTCCGCTATGGGAGCA 324


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Db 4 GGAACCTTTGGGAGGAGTCAGGCTCATGCTGCCCTGGAAACGAATCTCACCTTGC 63
QY 599 TTGAAAACTGAAGCGTCTCACAGCTACAAACCCGAAAGAGTTTGAAGTGAATCTGAAAA 658
Db 64 TAGAGAACTGAAGCGCTCACAGCTACAAACCCAGGAGCTTTGACTGGAACTGAAA 123
QY 659 GCGGGCGTGTTCATCATCAAGAGCTACTCTGAGGAGCAGCATCCACCGCTCCATTAAGT 718
Db 124 ATGACGCTGTGTTTATATAAAGAGCTATTCTGAGGATGATATCCACCGTTCCATCAAT 183
QY 719 ACTCCATCTGGTGTAGCAGACGACCGACAGCGCTGACAGCGCTTCGGCTGCA 778
Db 184 ACTCCATTTGGTGACGACAGCATGGGAATAACGCTGTGATAGCGCTATCCGCTCCA 243
QY 779 TGAGCAGCAAGGGCCCGCTTACCTGCTTTCAGCGTCAATGGGAGTGGGCAATTTTGTG 838
Db 244 TGAATGAAAGGCGCGCTTACCTCTGTTTACGCGTCAACGGCAGTGGACACTTCTGCG 303
QY 839 GGTGGCCGAGATGAATGCCCGCTGACTACGACAGTGCAGCGGGTCTGTGCTCAGG 898
Db 304 GCGTAGCCGAGATGAAGTCCCGCTGACTACGACAGTGCAGGCTGTCTGGTCAAGG 363
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Db 364 ACAATGGAAGGCGCAAGTTTGTGTCGGTGGCTGTGTGTCAAAGACGAGGGCAACACC 423
QY 959 AGTCCCGGCACATCAGGCTGTGAGAAATAACACAAACAAACCGGTCAACAACTCCCGGACA 1018
Db 424 AGTGATGCGCAGACGGGTGGAGCGGACACAGACACCGCGCGGCGGAGCGAGCG 483
QY 1019 CCCAGGAGTGCCTTA 1035
Db 484 CGCAGGAGTGCCTTA 500

RESULT 54
AW766493/c
LOCUS
DEFINITION
  da63c02.x1 Harland stage 19-23 Xenopus laevis cDNA clone
  IMAGE:3199586 3' similar to TR:064526 O64526 YUP8H12R.13 PROTEIN.
  ; mRNA sequence.
ACCESSION
  AW766493.1 GI:7698483
VERSION
  EST.
KEYWORDS
  African clawed frog.
SOURCE
  Xenopus laevis
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
    Xenopodinae; Xenopus.
REFERENCE
  Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
  Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
  ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
  Waterston,R. and Wilson,R.
  WashU Xenopus EST project, 1999
  Unpublished (1999)
  Other ESTs: da63c02.y1
CONTACT: Sandy Clifton, Ph.D.
  WashU Xenopus EST project, 1999
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@wustl.edu
  Library constructed by R. Harland, PhD.(University of California,
  Berkeley)
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: Xenopus clones from this library are available
  through the I.M.A.G.E. Consortium/LiNL at:
  image.llnl.gov/image/html/iresources.shtml
  Seq primer: -40UP from Gibco
  High quality sequence stop: 404.
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  Location/Qualifiers
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      /tissue_type="neurula"
      /dev_stage="stage 19-23"
      /lab_host="DH10B (phage-resistant)"
      /note="Vector: pCG107 (custom); Site 1: NotI; Site 2: SalI
      ; cDNA made by oligo-dT priming. Library constructed by
      Dr. Francesca Mariani in the laboratory of R. Harland,
      Ph.D. (University of California, Berkeley). References:
      XBP-2 is a transcriptional repressor that converts
      ectoderm into neural tissue. Mariani, F.V. Harland, R.M.,
      99030283. Use of large-scale expression cloning screens in
      the xenopus laevis tadpole to identify gene function.
      Grammer TC, Liu KJ, Mariani FV, Harland RM, Dev Biol.
      2000 Dec 15;228(2):197-210. PMID: 11112324; UI: 20564075;
      Note: This is a Xenopus Gene Collection (XGC) library."
BASE COUNT 146 a 147 c 127 g 168 t 4 others
ORIGIN
  Query Match 15.0%; Score 304.4; DB 2; Length 592;
  Best Local Similarity 79.4%; Pred. No. 7.2e-67;
  Matches 370; Conservative 0; Mismatches 95; Indels 1; Gaps 1;
  QY 691 GAGGAGCAGATCCACCGCTCCATTAAAGTACTCTGTTAGTACGAGCAGGACGCAAC 750
  Db 586 GAGCATGATATNTCTGCTTCCATTAAATATTTATGTGTTAGTATAGAGTATGGAAAT 527
  QY 751 AAGCGCTGGACAGCGCTTCCGCTGCATGAGCAGCAAGGGGCCCGTCTACCTGCTCTTC 810
  Db 526 ACATGCTTGGATAACGTTTTTTCGCTCTATGATGTTAAAGGCCCGGTTACTTCTCTTC 467
  QY 811 AGCGTCAATGGGAGTGGGCATTTTGTGGGTGGCCGAGATGAAGTCCCGCTGGGACTAC 870
  Db 466 AGCGTCAATGGCAGTGGATANTTTCTGTGGCGTAGCTGAGATGAAGTCTCTGTGGACTAT 407
  QY 871 GGACACAGTCCCGGGTCTGCTCAGGCAAGTGGAAAGGGAGTTTGTATGTCCAGTGG 930
  Db 406 GGACACAGTCCCGGGTGGTTCAGGACAAATGAAGGGCAAGTTTGTCAAGTGG 347
  QY 931 ATTTTGTTAAGGATGTACCCAAATAACAGCTCCGGCACAATCAGGCTGGAGATAACGAC 990
  Db 346 CTTTGTGTAAGGAGCTTCCCAACACAGCTCAGGCACATCCGCTGGAGATAACGAC 287
  QY 991 AACAAACCGTCAAAACTCCCGGACACCCAGGAGTGCCCTTAGAAAAGCCAAGCAA 1050
  Db 286 AACAAACCGTCAAAACTCCCGGACACCCAGGAGTGCCCTTAGAAAAGCAAACATG 227
  QY 1051 GTGCTGAATTTATCAGTCTTCAACAGCACACAACCTCCATCTTTCGACGACTTGTCTC 1110
  Db 226 GTGCTTAAATCATTTGCCACTTAAAGACACACGACCTCCATCTTTGATGACTTTTCTCAT 167
  QY 1111 TAGCAGAAGCGCCA-GAGGAGGAGGAGTGGTGGCAAGGAACGCGC 1155
  Db 166 TAGCAGAAGCGCGCAGGAGGAGGAGTGGTGGCAGGTAACGC 121
RESULT 55
AJ453895
LOCUS
DEFINITION
  AJ453895 riken1 Gallus gallus cDNA clone 35o2r1, mRNA sequence.
ACCESSION
  AJ453895
VERSION
  AJ453895.1 GI:20263991
KEYWORDS
  EST.
SOURCE
  chicken.
  ORGANISM
    Gallus gallus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
    Phasianinae; Gallus.
```



```

REFERENCE
AUTHORS      Buerstedde,J.M.
TITLE        Gallus gallus bursal lymphocyte EST
JOURNAL      Unpublished (2002)
COMMENT      Contact: Buerstedde JM
              Cellular Immunology
              Heinrich-Pette-Institute
              Martinstr. 52, 20251 Hamburg, Germany
              Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES
source
1..732
    /organism="Gallus gallus"
    /db_xref="taxon:9031"
    /clone_lib="f502r1"
    /cell_type="bursal lymphocyte"
    /dev_stage="2-3 weeks old"
    /note="CB inbred strain"

BASE COUNT      201 a 173 c 168 g 190 t
ORIGIN
Query Match      14.9%; Score 301.8; DB 1; Length 732;
Best Local Similarity 82.7%; Pred. No. 3.5e-66;
Matches 345; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 1 CAAAAGCACAAGATAATAAGTACAAAATGGTTTCGTTACATCAGAAGGATACAGTTTCATG 60
Db 100 CGAAAGGACAGGATAATAAGTACAAAATGGTTTCGTTACATCAAAAGGATACAGTTTCACG 159
QY 61 ACAATGACTTTGAGCCCTACCTTACTGGCAGTCACAAATCAGATTAACAGTTTACCCCTCAA 120
Db 160 ACAACGATTTTGAACCTTACCTTTCTGGCAGTCACAAATCAGATTAACAGTTTACCTCAA 219
QY 121 TGAGCGACCCCTACCTGTGCAGCTATTACCCGCGTCCATTGGATTTCTTACTTCCCTCA 180
Db 220 TGACTGATCCTTATCTGTCAAGTTATTATCCACATCTATCGGGTTTCCCTACTCTCTCA 279
QY 181 ATGAGGCTCCGTGGTCTACTGCAGGGACCCCTCCGATTTCATACCTACCAACCTACGGAC 240
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QY 241 AGCTCAGTAACGGAGACCATCATTTTATGACAGATGCTGTGTTTTGGGAGGCTGGGGGCC 300
Db 340 AGCTCAGTAATGGAGATCATCATTTTATGATGATGCTGTGTTTTGGACAGGCTGGGGGTC 399
QY 301 TGGGGAACAACATCTATCAGACACAGGTTCAATTTTTTCCCTGAAACCCCTCGTTCTCAG 360
Db 400 TGGGAATATATATCTATCAACCGGTTTAATTTTTTCCCTGAAATCTCGCTTCTCAG 459
QY 361 CATGGGGACAAGTGGGTCTCAAGGTACAGACACCCAGAGCTCAGGCTTCTCCCAAGCA 417
Db 460 CTTGGGGAACAAGTGGATCCCAAGGACAGACAGACTCAAAGTTCAGCATATGGGAGCA 516

RESULT 56
AA099707
LOCUS
DEFINITION      zH86a12.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:489694 5', mRNA sequence.
AA099707
ACCESSION
VERSION
KEYWORDS
SOURCE
    Homo sapiens
    Sukaryaota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1 (bases 1 to 421)
    Hillier,L., Lennon,G., Becker,M., Bonaudo,M.F., Chiapelli,B.,
    Chissoe,S., Dietrich,N., DuBucque,T., Favello,A., Gish,W., Hawkins
    ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
    ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
    Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaszka,E.,
    Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
    EST.
    AA099707.1 GI:1645799
    EST.
    Homo sapiens
    Homo sapiens

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TITLE Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL Genome Res. 6 (9), 807-828 (1996)
 MEDLINE 97044478
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.lml.gov) for further information.
 Insert Length: 811 Std Error: 0.00
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 360.
 Location/Qualifiers
 1. .421
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 /db_xref="taxon:9606"
 /clone="IMAGE:489894"
 /clone_lib="Soares_pregnant_uterus_NbHPU"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: p7T73-Pac; Site 1: Not I;
 Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer [5',
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 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified p7T73 vector. Library
 went through one round of normalization. Library
 constructed by M. Fatima Bonaldo."
 BASE COUNT 97 a 70 c 94 g 156 t 4 others
 ORIGIN
 Query Match 14.8%; Score 300.4; DB 1; Length 421;
 Best Local Similarity 98.2%; Pred. No. 6.9e-56;
 Matches 323; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
 QY 1700 CTGCTAGACAGATAACTTTTAATTTTCAAAATTTGGCAGACACTTTTTTTTTTTTTTTGA 1759
 DB 1 CTCTAGACAGATAACTTTTAATTTTCAAAATTTGGCAGACACTTTTTTTTTTTTTTTGA 59
 QY 1760 AAATCTTTTCCTCCAGATCTGTTGCCCACTGAACAGACCACCGTCCCTCACTGTCCTGGT 1819
 DB 60 AAATCTTNCCTCCAGATCTGTTGCCCACTGAACAGACCACCGTCCCTCACTGTCCTGGT 119
 QY 1820 GTCGATTTGGGCTGGATGTTGTTGGGGCATGATGTGTGGAGGAACCTGGAAGGTGCTTTAG 1879
 DB 120 GTCGATTTGGGCTGGATGTTGTTGGGGCATGATGTGTGGAGGAACCTGGAAGGTGCTTTAG 179
 QY 1880 GTCGTGTTCAAGGTTCGGGCATCTTTGTTGCTTTTGCACATCTTTTAAATTTTACACCTTT 1939
 DB 180 GTCGTGTTCAAGGTTCGGGCATCTTTGTTGCTTTTGCACATCTTTTAAATTTTACACCTTT 239
 QY 1940 TCTTAAGAAATCTTAATGCCGCTTAAGTTTTTATACCAATAAGCTGAGCTTTAAGTGT- 1998
 DB 240 TCTTAAGAAATCTTAAGGCCGCTTAAGTTTTTATACCAATAAGCTGAGCTTTAAGTGT 299
 QY 1999 AGGATCTGGTAGTACAGACAGTGTGATGG 2027
 DB 300 AGGATCTGGTAGTACAGACAGTGTGATGG 328
 RESULT 57
 AJ397688
 LOCUS AJ397688 dkfz426 Gallus gallus cdna clone 30j10r1, mRNA sequence. EST 25-JAN-2001
 DEFINITION
 ACCESSION AJ397688
 VERSION AJ397688.1 GI:7130878
 KEYWORDS EST.
 SOURCE chicken.

ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 741)
AUTHORS Abdrakmanov,I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy
J., Korn,B. and Buerstedde,J.M.
TITLE A large database of chicken bursa ESTs as a resource for the
analysis of vertebrate gene function
JOURNAL Genome Res. 10 (12), 2062-2069 (2000)
MEDLINE 20568495
COMMENT Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institut
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: <http://genetics.hpi.uni-hamburg.de/dt40est.html>.
FEATURES
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1..741
/organism="Gallus gallus"
/strain="CB"
/db_xref="taxon:9031"
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Best Local Similarity 76.9%; Pred. No. 9e-66;
Matches 379; Conservative 0; Mismatches 113; Indels 1; Gaps 1;
Qy 693 GGAGCATCCACCGCTCCATTAGTACTCCATCTGTGTAGCAGACGACGCAACAA 752
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Qy 753 GCGCTTGACAGCGCTTCGCTGCATGAGCAGCAAGGGGCCCTTACCTGTCTTCAG 812
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Qy 873 CACAGTGGCGGGTCTGGTCTCAGGACAGTGAAGGGAAGTTTGTATGTCCAGTGGAT 932
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Qy 993 CAACCGGTCAAACTCCCGGGACACCCAGGAGTGGCCCTTGAAGAAAGCAAGCAAGT 1052
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Qy 1053 GCTGAAATATCAGTTCTTACAGCAGACAACTCCATCTTTCGACGACTTGTCTACTA 1112
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Qy 1113 CGAAGCGGCA-CAGGAGGAGGAGTGGTGGCGCAAGCAAGCGGAGAGTGCAGAAACA 1171
Db 421 TGAGAACGCCAGAGGAGGAGGAGAACTGTTAAAGAGCAAGCGGCGGTGTCAATA 480
Qy 1172 ATGAGGCGGAAC 1184
Db 481 GAAGGCGCATCCC 493
RESULT 58
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LOCUS

DEFINITION vrl8d03.y1 Barstead mouse myotubes MP1RB5 Mus musculus cDNA clone
IMAGE:1120997 5', mRNA sequence.
ACCESSION A1604044
VERSION A1604044.1 GI:4613206
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 487)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:610333
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 470.
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/strain="C3H"
/db_xref="taxon:10090"
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/cell_line="C2C12"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
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was primed with a Not I - oligo(dT) primer [5'
TGTTAGCAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATCGGATCTGT], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."
BASE COUNT 114 a 143 c 117 g 113 t
ORIGIN
Query Match 14.8%; Score 300; DB 1; Length 487;
Best Local Similarity 89.0%; Pred. No. 9.1e-66;
Matches 324; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
Qy 1 CAAAGGACAAGATAATAAGTACAAATGGTTCGTATCATCAGAGGATACAGTTTCATG 60
Db 124 CAAAGGACAAGATAATAAGTACAAATGGTTCGTATCATCAGAGGATACAGTTTCATG 183
Qy 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGAGTAAACAGTTACCCCTCAA 120
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Db 244 TGAGTGATCCTTACCTGTCCAGTTACTATCCACCATCCATTGGATTTCCTTACTCCCTCA 303
Qy 181 ATGAGGCTCGGTGCTACTGCGAGGGGACCCCTCGATTCCATACCTCACCACCTACCGAC 240
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QY 241 AGCTCAGTAACGAGACCATCATCTTTTATGACGATGCTGTTTTTGGGCGACCTGGGGGCC 300
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QY 301 TGGGGAACAACATCTATGACGACAGGTTCATTTTCCCTGAAACCCCTGGTTCTCAG 360
Db 424 TGGGGAACAACATCTTACGACGACAGGTTCATTTTCCCTGAAACCCCTGATTTCTCAG 483
QY 361 CATG 364
Db 484 CATG 487

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DEFINITION 601060774F2 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447139 5',
mRNA sequence.
ACCESSION BE540016
VERSION BE540016.1 GI:9768661
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM8420 row: d column: 20
High quality sequence stop: 626.
Location/Qualifiers
1..752
/organism="Homo sapiens"
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/clone="IMAGE:3447139"
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/cell_line="MGC36"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
Technologies."

BASE COUNT 211 a 163 c 197 g 181 t
ORIGIN
Query Match 14.7%; Score 298.4; DB 2; Length 752;
Best Local Similarity 73.6%; Pred. No. 2.6e-65;
Matches 434; Conservative 0; Mismatches 151; Indels 5; Gaps 4;

QY 583 GAATCCACCCCGCTCTTGAAGAACTGAGAGCTGCTCACAGCTACACCCGAAAGAGTTT 642
Db 83 GAACCCACCCAGTGTGGAGAGCTTCGGTCCATTAATACTAATACCCCAAGATTTT 142
QY 643 GAGTGAATCTGAAACGGGGCTGTGTTTCATCATCAAGAGCTACTCTGAGGACGATC 702
Db 143 GACTGGAATCTGAAACATGCGCGGGTTTTCATCATTAAGAGCTACTCTGAGGACGAT 202
QY 703 CACCGCTCCATTAGTACTCCATCTGCTGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 762
Db 203 CACCGTTCCATTAGTATAATATTTGGTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 262
QY 763 AGCGCCTTCGCTGCATGAGCAGCAGGCGCGCTCTACCTGCTCTTCAGCGTCAATGGG 822
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Db 263 GCTGCTTATCGTTTCATGAACGGGAAAGGCCCGTTTACTTTTTCAGTGTCAACGCC 322
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Db 323 AGTGGCACTTCTGTGGGCTGGCAGAAATGAATCTGCTGTGGACTACAACATGTGCA 382
QY 883 GGGGTCTCGTCTCAGGACAAGTGGGGAAGTTTGTATGTCCAGTGGATTTTGTGTAAG 942
Db 383 GGTGTGCTGCTCCAGGACAAATGGAA-GGGTCTGTTTGTATGTCTCAGGTGGA-TTTTGTGAAG 440
QY 943 GATGTACCCCAATACCACTCCGCGCACATCAGGCTGGAGATAACGACAAACAAACCGGTC 1002
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QY 1003 ACAAACTCCCGGACACCCAGGAGTGCCTTTAGAAAAAGCCAAAGTGTGTAATAAT 1062
Db 501 ACCAACTCTAGGACACTCAGGAAGTGCCTCTGGAAAAAGGCTA--GCAGGTGTGAATAAT 558
QY 1063 ATCAGTCTCTACAGCACACAACTCCATCTTCGAGAGCTTTTGTCTCAGTACGAGAGCGC 1122
Db 559 ATAGCCAGCTACAGCACACCACTTCCAT-TTTGTATGACTTCTCACACTATGAGAAACGC 617
QY 1123 CAGAGGAGGAGGAGTGTGCGCAGGAAACGCGCAGTGCAGAAACAAACAA 1172
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RESULT 60
LOCUS AL584855 630 bp mRNA linear EST 28-FEB-2001
DEFINITION AL584855 Stratagene Chick Embryo Lambda cDNA Library (* 937405)
Gallus gallus cDNA clone ROS015C08, mRNA sequence.
ACCESSION AL584855
VERSION AL584855.1 GI:13163588
KEYWORDS EST.
SOURCE Gallus gallus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 630)
Murray.F.
Stratagene Chick Embryo Lambda cDNA Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbserc.ac.uk
Seq primer: T3
Location/Qualifiers
1..630
/organism="Gallus gallus"
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937405)"
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/lab_host="SOLR cells (kanamycin resistant)"
/note="Vector: pBLUESCRIPT SK; Site 1: EcoRI; Site 2: XhoI
; Cloned unidirectionally. Primer: Oligo dT. Uni-ZAP XR
vector. Average insert size: 1.5kb.; 5' adaptor sequence:
5' GAATTCGGCAGCAG 3'; 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTT 3'."

BASE COUNT 201 a 116 c 142 g 169 t
ORIGIN
Query Match 14.7%; Score 298.2; DB 1; Length 630;
Best Local Similarity 75.5%; Pred. No. 2.8e-65;
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Matches 383; Conservative 0; Mismatches 123; Indels 1; Gaps 1;
QY 667 GTGTTTCATCATCAAGAGCTACTCTGAGGACGACATCCACCGCTCCATTAACTACTCCATC 726
Db 15 GTGTTTATAATCAAAAGTTATTCAGAGGACGATATTCATCGCTCCATTAACTACTCTATC 74
QY 727 TGTGTAGCAGACAGCGGCAACAGCGCTGGACAGCGCTTCCGCTGATGAGGAGC 786
Db 75 TGTGTGTAGTACTGAACATGTAATAAGCGCTTGGATGCTGTACCGTTCCTTGAATGGA 134
QY 787 AAGGGCGCGTCTACCTGCTCTTCAGCGCTCAATGGAGTGGGCAATTTTGTGGGGTGGCC 846
Db 135 AAAGCGCGCTCTATTACTCTTCAGTGTGAATGGAGTGGACACTTTTGTGGAGTGGCT 194
QY 847 GAGATGAAGTCCCCCGTGGACTACGGCACCAGTGC CGGGGTCTCGTCTCAGGACAAGTGG 906
Db 195 GAGATGAAGTCTGTGTGGACTACAATGTCATATGCTGCGCTCTGCTCAGGATAAGTGG 254
QY 907 AAGGGGAAGTTTGATGTCTCAAGTATTTTGTAAAGNATGTAACCAATTAACCAAGTCCGG 966
Db 255 AAGGGCAAGTTTGATGTCAAAATGGATCTTTGTCAAGACGTTTCCCAATAACCAACTCGG 314
QY 967 CACATCAGGCTGGAGATAACGACCAACAAACCGGTCAACAATCTCCGCGGACCCAGGAG 1026
Db 315 CATATTGCTTGGAAACAATGACAAACAACAGTTTCAAAATTCGAGGACACTCAAGAA 374
QY 1027 GTGCCCTTAGAAAAAGCAAGCAAGTGTGAAAAATTAATCAAGTCTTCAAGCACACAACC 1086
Db 375 GTACCCCTAGAAAAAGCAAGCAAGTGTGAAAAATTAATCAAGTCTTCAAGCATACCACC 434
QY 1087 TCCATCTTCAGACGACTTTGCTACTACGAGAAAGCG-CCAGAGGAGGAGGAGTGGTGGCG 1145
Db 435 TCAATCTTGTATGACTTTGTCATATTATGAAAGCGTCAAGAAAGGAGGAGGAGGATCGT 494
QY 1146 AAGGAAGCGAGAGTCGAAACAAACA 1172
Db 495 AGGAGAGGAATAGAAACAACAATAA 521

RESULT 61
BE375521
LOCUS
DEFINITION
60125407F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3584040 5',
mRNA sequence.
BE375521
ACCESSION
VERSION
BE375521.1 GI:9320886
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 612)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: L14M8741 row: m column: 01
High quality sequence stop: 590.
Location/Qualifiers
1. .612
/organism="Mus musculus"
/strain="FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:3584040"
/clone_lib="NCI_CGAP_Mam1"

FEATURES
source
```

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/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: Sali;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 204 a 107 c 135 g 166 t
ORIGIN
Query Match 14.6%; Score 295.8; DB 2; Length 612;
Best Local Similarity 70.8%; Pred. No. 1.1e-64;
Matches 407; Conservative 0; Mismatches 167; Indels 1; Gaps 1;
QY 620 ACAGCTACAAACCCGAAAGAGTTTTCAGTGGAAATCTGAAAGCGGCGGTGTTCATCATCA 679
Db 1 ACAATTATATCCCAAGAGACTTTGATTGGAACTGGAAGATGGACGTGTGTTTATATTA 60
QY 680 AGAGCTACTCTGAGGAGCAGATCCACCGCTCCATTAAGTACTCTCATCTGCTGTGTAGCACAG 739
Db 61 AGAGCTATTCTGAGGATGATATACATCGTTCATCAAGTACTCTATCTGCTGTAGTACTG 120
QY 740 AGCAGCGACACAGCGCTCGACAGCGCTTCCGCTGCATGAGCAGCAAGGGGCCCTCT 799
Db 121 AGCATGTAATAAGCGTTTGGATGCAAGCTTATCGTTCCTCGAATGGGAAAGGCCACTCT 180
QY 800 ACCTGCTCTTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGGTGGCCGAGATGAAGTCCC 859
Db 181 ATTACTCTTCAGTGTGAATGGCAGTGGACATTTTGTGGAGTGGCTGAAATGAAGTCTG 240
QY 860 CCGTGGACTACGGCACAGTCCCGGGGTCTGGTCTCAGGACAAAGTGGAAAGGGGAAGTTTG 919
Db 241 TTGTAGACTATAATGCTTATGCTGGTCTGCTCAGGATAAGTGGAGGGCAAAATTTG 300
QY 920 ATGTCAGTGGATTTTGTAAAGATGTACCAATTAACAGCTCCGCGCACATCAGGCTGG 979
Db 301 AAGTTAAATGGATCTTTGTCAAAGATGTTCCCAATTAACCAATTAACGACATATTGCGCTTAG 360
QY 980 AGAATAACGACAAACAAACCGGTCAAAACTCCCGGGACACCCAGGAGGTGCCCTTAGAAA 1039
Db 361 AAAATAATGACACAAACCAAGTAAACCAATTCAGGGNACATCAAGAGTACCCTTAGAAA 420
QY 1040 AAGCAAGCAAGTGTGAAATTAATATCAGTTTC-CTAAGCAGCACACAACTCCATCTTCGAC 1098
Db 421 AAGCAAGCAAGTGTGAAATTAATATCAGTTTC-CTAAGCAGCACACAACTCCATCTTCGAT 480
QY 1099 GACTTTGCTCACTACGAGAGCGCCAGAGGAGGAGGTGGTGGCGCAAGGAGCGGAGA 1158
Db 481 GACTTTCACATTAATGAAAGCGTCAAGAGGAGGAGGAGGAGGAGGAGGAGAGACATA 540
QY 1159 GTGAAACAAACAAATGAGGGCGAAACCAAGTTTCTTA 1193
Db 541 GAAACAAGCAATAACCAACCGTGTGGAGATGTCCTA 575

RESULT 62
BB654392
LOCUS
DEFINITION
BB654392 RIKEN full-length enriched, 2 days neonate thymus thymic
cells Mus musculus cDNA clone C920004N12 5', mRNA sequence.
BB654392
ACCESSION
VERSION
BB654392.1 GI:16488220
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 637)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hasegawa, T., Hara, A.,
Hiramoto, K., Hori, Y., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Sasaki
Okazaki, Y., Okido, T., Saito, K., Sakai, K., Sano, H., Sasaki
D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
```

Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)

TITLE
JOURNAL
COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suihoro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayashizaki, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, K. I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

e mouse tissues.

FEATURES
source

Location/Qualifiers

1. 637
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C920004N12"
/clone_lib="RIKEN full-length enriched, 2 days neonate thymus-thymic cells"
/tissue_type="thymus"
/cell_type="thymic cells"
/dev_stage="2 days neonate"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT) -Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

BASE COUNT 121 a 210 C 170 G 136 T

ORIGIN

Query Match 14.5%; Score 294.2; DB 2; Length 637;
Best Local Similarity 89.4%; Pred. No. 2.9e-64;

Matches 328; Conservative 0; Mismatches 38; Indels 1; Gaps 1;
Qy 1 CAAAAGGACAAAGATAAATAAGTACAAAATGGTTCGTACATCAGAAGATACAGTTTCATG 60
Db 271 CAAAAGGACAAAGATAAATAAGTACAAAATGGTTCGTACATCAGAAGATACAGTTTCATG 330
Qy 51 ACAATGACTTTGAGCCCTACCTTACTGACAGATCAATACAGTAACAGTTTACCCCTCAA 120
Db 331 ACAATGACTTTGAGCCCTACCTTACTGACAGATCAATACAGTAACAGTTTACCCCTCGA 390
Qy 121 TGAGGACCCCTACTGTCCAGCTATTACCCGCGCTCCATTGGATTTCCTTACTCCCTCA 180
Db 391 TGATGATCCCTACTGTCCAGTACTATCCACCATCCATTGGATTTCCTTACTCCCTCA 450
Qy 181 ATGAGGCTCCGTGTACTACTGAGGGACCCCTCCGATTCCTACCTACCTACCGGAC 240
Db 451 GCGAGGACCATGGTCCACTGCGAGGGACCCCTCCCATCCGTATCTCACTACCTATGGAC 510
Qy 241 AGCTCAGTAACGGAGACCATCATTTTATGACGATGCTTTTGGGAGCCTGGGGGCC 300
Db 511 AACTTAGTAAATGGAGACCATCACTTCATGCATGATGCTTTTGGGAGCCTGGGGGTC 570
Qy 301 TGGGAAACAAATCTATCAGCACAGG-TTCAATTTTTTCCCTGAAAACCTCGCTTCTCA 359
Db 571 TGGGAAACAAATCTATCAGCACAGGTTTTATTTTTTCCCTGAAAACCTCGCTTCTCA 630
Qy 360 GCATGGG 366
Db 631 GCATGGG 637

RESULT 63
AA323869
LOCUS AA323869 316 bp mRNA linear EST 20-APR-1997
DEFINITION EST26711 Cerebellum II Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION AA323869
VERSION AA323869.1 GI:1976196
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkie, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.W., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudke, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kusch, C., Hungjun, J., Li, H., Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Hasseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

TITLE
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)

JOURNAL
MEDLINE
COMMENT

Other_ESTs: THCI92215
Contact: Kerlavage, AR

Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423

Email: arkerlav@igr.org
For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers

1..316

/organism="Homo sapiens"

/db_xref="ATCC (inhost):124420"

/db_xref="taxon:9606"

/clone_lib="Cerebellum II"

/tissue_type="cerebellum"

/dev_stage="adult"

/notes="Organ: brain; Vector: pBluescript SK-; Site_1:

EcoRI; Site_2: XhoI"

88 a 80 c 87 g 56 t 5 others

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 97.1%; Score 287.2; DB 1; Length 316;

Matches 300; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

851 TGAAGTCCCGCTGCTACGGCACCACTGCGGGGTCTGCTCTCAGGACAAGTGAAGG 910

8 TGAAGTCCCGCTGCTACGGCACCACTGCGGGGTCTGCTCTCAGGACAAGTGAAGG 67

911 GGAAGTTTGATGTCAGTGGATTTTGTAAAGATGTACCAATPAACCAAGTCCGGCACA 970

68 GGAAGTTTGATGTCAGTGGATTTTNTAAAGATGTACCAATPAACCAAGTCCGGCACA 127

971 TCAGGCTGGAGATTAAGCACAAACCGGTCAAACTCCGGGACACCGAGAGTGC 1030

128 TCAGGCTGGAGATTAAGCACAAACCGGTCAAACTCCGGGACACCGAGAGTGC 187

1031 CTTTAAAGAAAGCCCAAGCAAGTGTGAAATTTATCAGTTCTTACAAGCACACCACTCCA 1090

188 CTTTAAAGAAAGCCCAAGCAAGTGTGAAATTTATCAGTTCTTACAAGCACACCACTCCA 247

1091 TCTTCGACGACTTTGCTCACTACGAGAGCGCCA-GAGGAGGAGGAGTGTGCGCAAGG 1149

248 TCTTCGACGACTTTGCTCACTACGAGAGCGCCAAGGAGGAGGAGTGTGCGCAAGG 307

1150 AACGGCAGA 1158

308 AACGGCAGA 316

RESULT 64

AJ447891

LOCUS

DEFINITION AJ447891 riken1 Gallus gallus cDNA clone 18a13r1, mRNA sequence.

ACCESSION AJ447891

VERSION AJ447891.1 GI:20215112

KEYWORDS EST.

SOURCE chicken.

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 616)

Buerstedde, J.M.

Gallus gallus Bursal lymphocyte EST

Unpublished (2002)

CONTACT: Buerstedde JM

Cellular Immunology

Heinrich-Pette-Institute

Martinistr. 52, 20251 Hamburg, Germany

Email: URL: <http://genetics.hpi.uni-hamburg.de/dt40est.html>.

Location/Qualifiers

1..616

/organism="Gallus gallus"

/db_xref="taxon:9031"

/clone="18a13r1"

/clone_lib="riken1"

/cell_type="bursal lymphocyte"

FEATURES

source

/dev_stage="2-3 weeks old"

/notes="CB inbred strain"

BASE COUNT 143 a 186 c 140 g 144 t 3 others

ORIGIN

Query Match 14.0%; Score 284.8; DB 1; Length 616;

Best Local Similarity 82.5%; Pred. No. 7.1e-62;

Matches 325; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 CAAAGGCAAGATAATTAAGTCAAAATGGTTCTGTACATCAGNAGGATACAGTTTCATG 60

Db 196 CGAAGGACAGGATAATAAGTCAAAATGGTTCTGTACATCAAAAGGATACAGTTTCACG 255

QY 61 ACAATGACTTTTGAGCCCTACCTTACTGGACAGTCAATCAGAGTAAACAGTTACCCCTCAA 120

Db 256 ACAACGATTTTGAACCTTACCTTCTGGGAGTCAATCAGACAGTAGTATCCATCAA 315

QY 121 TGAGGACCCCTACCTGTCAGTTCAGTATTAACCCGCGTCCATTTGGATTTCCTTACTCCCTCA 180

Db 316 TGACTGATCCTTATCTGTCAAGTTATTATCCACCACTATTGGGTTTCCCTACTCTCTCA 375

QY 181 ATGAGGCTCGTGTCTACTGTCAGGGACCCCTCGGATTCATACCTCACCACCTACGGAC 240

Db 376 GTGAAGCGCCATGGTCTACAGGAGGAGATCCTCTATCCGATATCTCACCACTATGGAC 435

QY 241 AGCTCAGTAACGAGACCATCATTTTATGCAGATGCTGTTTTGGGAGCCCTGGGGGCC 300

Db 436 AGCTCAGTAATGAGATCATTTTATGCATGATGCTGTTTTGGACAGCCCTGGGGGTC 495

QY 301 TGGGGAAACAATCTATCAGCACAGGTTCAATTTTTTCCCTGAAAAACCCCTGCGTTCTCAG 360

Db 496 TGGGAAATAATCTATCAACACCGGTTTAACTTTTCCCTGAAAAATCCTGCGTTCTCAG 555

QY 361 CATGGGGCAAGTGGTCTCAAGGTCAGCAGAC 394

Db 556 CTTGGGGAACAAGNGGATCCAGGGCNGGAAGAC 589

RESULT 65

AA977084/c

LOCUS

DEFINITION

AA977084.1

GI:3154530

EST.

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 679)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/BLN at:

www-bio.lnlnl.gov/bbrp/image/image.html

Seq primer: -40ml3 fwd. ET from Amergham

High quality sequence stop: 459.

Location/Qualifiers

1..679

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1587173"

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/clone_lib="NCI_CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

BASE COUNT      169 a 162 c 133 g 215 t
ORIGIN
Query Match      14.0%; Score 284; DB 1; Length 679;
Best Local Similarity 74.0%; Pred. No. 1.2e-61;
Matches 373; Conservative 0; Mismatches 130; Indels 1; Gaps 1;

QY 670 TTTCATCATCAAGAGCTACTCTGTAGGAGGACATCCACCGCTCCATTAAAGTACTCCATCTGG 729
Db 679 TTTCATCATTAAGAGCTACTCTGTGGACGATATTTCCACGTTCCATTAAAGTATAATATTGG 620

QY 730 TGTAGCACAGAGCAGCGCAACAGCGCTGGACAGCGCTTCGCTGCATGAGCAAG 789
Db 619 TGCAGCAGGAGCATGGTAAACAGAGACTGGATGCTGCTTATCGTTCCATGAACGGGAAA 560

QY 790 GGGCCCGTCTACCTGCTCTTACAGCGTCAATGGAGTGGGCAATTTTGTGGGTGGCCGAG 849
Db 559 GGGCCCGTCTTACTTCTTTCAGTGTCAACGGCAGTGGACATCTCTGTGGCGTGGCAGAA 500

QY 850 ATGAAGTCCCGGTGACTACGGCAACAGTGGCGGGTCTGTTCTCAGCAACAGTGGAG 909
Db 499 ATGAATCTGCTGTGACTACACACATGTCAGAGTGTGTGGTCCCGAGCAAAATGGAAG 440

QY 910 GGGAGCTTTGATGTCAGTGGATTTTGTAGGAGTATCCCAATACAGCTCCGGCAC 969
Db 439 GGTGCTTTTGTATGTCAGTGGATTTTGTAGGAGCTTCCCAATAGCCAATGCGACAC 380

QY 970 ATCAGCGTGGAGAAATACGACAAACCGGTCAACAACTCCCGGACACCCAGGAGGTG 1029
Db 379 ATTGCGCTAGAGAACACGAGATTAACCGATGACCACTCTAGGACACTCAGGAAGTG 320

QY 1030 CCTTTAGAAAAAGCCAGCAAGTGTGTAATAATTATCAGTTCTTACAGCACACAACTCC 1089
Db 319 CCTCTGAAAAAGGCTAAGCAGGTGTTGAAAAATTATAGCCAGCTACACAGCACACCACTTC 260

QY 1090 ATCTTCAGCAGCTTCTCTACTAGCAGAGCGCC-AGAGGAGGAGGAGTGGTGCCGCAAG 1148
Db 259 ATTTTGTATGACTTCTCACACTATGAGAACGCCAAGAGAGGAAGAAAGTGTTAAAAAG 200

QY 1149 GAACGGCAGAGTCGAAACAAACAA 1172
Db 199 GAACGTCAGGTCGTGGAAATAA 176

RESULT 66
AL627746      689 bp mRNA linear EST 02-NOV-2001
LOCUS
DEFINITION
AL627746      XGC-gastrula Silurana tropicalis cDNA clone Tgas025h05 5',
mRNA sequence.
ACCESSION
AL627746      GI:16597229
VERSION
AL627746.1
KEYWORDS
EST.
SOURCE
western clawed frog.
ORGANISM
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 689)
REFERENCE
Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
JOURNAL
Unpublished (2001)
COMMENT
Contact: Huckle E
```

```
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: Tgas025h05.sp6
Sequencing_primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
source      1..689
            /organism="Silurana tropicalis"
            /db_xref="taxon:8364"
            /clone="Tgas025h05"
            /clone_lib="XGC-gastrula"
            /dev_stage="gastrula (stages 10.5-13 mixed)"
            /lab_host="Escherichia coli XL1-blue"
            /note="vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
            was oligo dT primed from sug of poly A+ RNA then ligated
            10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
            into pCS107 with EcoRI at the 5' end and NotI at the 3'
            end."

BASE COUNT    139 a 253 c 166 g 129 t 2 others
ORIGIN
Query Match    13.6%; Score 274.8; DB 1; Length 689;
Best Local Similarity 79.4%; Pred. No. 2.6e-59;
Matches 324; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 CAAAGGACAGATATAAGTACAAAATGGTTGTTATCATCAGAGGATACAGTTTCATG 60
Db 243 CAAACAATGATCTTATTTTCAGTTCAAAACGGATCCCTGCACCAGAGGACAGCGTGACG 302

QY 61 ACAATGACTTTTGGGCGCTTACTTGGACAGTCAAATCAGAGTAACAGTTACCCCTCAA 120
Db 303 ATATGACTTCGAGCAGTACCTGTGCGGACAGTCCCAATCAGAGTAACAGTACCCCTCCA 362

QY 121 TGAGGACACCCCTACCTGTCCAGCTATTACCGCCGTCATGGATTTCTTACTCCCTCA 180
Db 363 TGACCGACCCGTCACCTGTCCAGTTACTACCCCTCTTCTATCGGCTTTCCGTATTGCTCA 422

QY 181 ATGAGCTCCGTGGTCTACTGTGAGGGAGCCCTCCGATTCATCCATCCACACCTACGGAC 240
Db 423 GGAAGCTCTCTTGGTCAACCGCGGGGACCCCGGATCCGCTACCTACCCCGTACGGAC 482

QY 241 AGCTCAGTAACCGAGACCATCATTTTATGCAGCATGCTGTTTTTGGGAGCCTTGGGGGCC 300
Db 483 AGCTCAGCAACCGAGACCCACCATTTTCATGCAGATGCGTCTTTGGGAGCCCGCGGCC 542

QY 301 TGGGAAACAACTCTATCAGCAGAGTTTCAATTTTTTCCCTGAAAAACCCCTGGTCTCAG 360
Db 543 TGGGAAATAACATCTATCAGCACCGGTTCAACTTCTTCCCGGAAAAACCCAGCCTTTTCG 602

QY 361 CATGGGGAACAGTGGTCTCAAGTCCAGCTCAGCAGACCCAGAGCTCAGCCT 408
Db 603 CATGGGGAGCAGCGGCTCCCGANGGCGAGCAGACCCAGAACTCCGCT 650

RESULT 67
AL398704      447 bp mRNA linear EST 12-AUG-1997
LOCUS
DEFINITION
AL398704      zt70h04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727735
3', mRNA sequence.
ACCESSION
AL398704
VERSION
AL398704.1
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
REFERENCE
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
```

.TITLE T., Waterston, R. and Wilson, R.
 JOURNAL WashU-Merck EST Project 1997
 COMMENT Unpublished (1997)
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 831 Std Error: 0.00
 Seq primer: -41m13 fwd. ET from Amersham
 High quality sequence stop: 436.

FEATURES

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 /organism="Homo sapiens"
 /db_xref="GDB:5924646"
 /db_xref="taxon:9606"
 /clone="IMAGE:727735"
 /clone_lib="Soares_testis_NHT"
 /sex="male"
 /lab_host="DH10B"
 /note="Vector: p7T3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from Clontech Laboratories
 Inc. and primed with a Not I - oligo(dT) primer [5',
 TGTTACCAATCTGAATGGAGGCGCGCCCAATTTTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified p7T3 vector. Library
 went through one round of normalization to Cot5, and was
 constructed by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 103 a 75 c 111 g 158 t

ORIGIN

Query Match 13.5%; Score 274; DB 1; Length 447;
 Best Local Similarity 100.0%; Pred. No. 3,7e-59;
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1755 TTTGAAATCTTCTCCAGATCTGTGGCCACTGAACGCCACCGTCCCTCACTGTC 1814
 Db 1 TTTGAAATCTTCTCCAGATCTGTGGCCACTGAACGCCACCGTCCCTCACTGTC 60
 QY 1815 CTGTGTCCGATTCGGCTGGATGTGTGGGCGATGATGTGGAGCACTGGAAGTGC 1874
 Db 61 CTGTGTCCGATTCGGCTGGATGTGTGGGCGATGATGTGGAGCACTGGAAGTGC 120
 QY 1875 TTTAGGTCTGTTCCAGGTCCGGGCACTTTTGTGTTTGCACATCTTTTAAATTTTACA 1934
 Db 121 TTTAGGTCTGTTCCAGGTCCGGGCACTTTTGTGTTTGCACATCTTTTAAATTTTACA 180
 QY 1935 CTTTCTTAAAGATTTCTAATGCGGCTTAAGTTTATATACCAATATAGTGCAGCTTTAA 1994
 Db 181 CTTTCTTAAAGATTTCTAATGCGGCTTAAGTTTATATACCAATATAGTGCAGCTTTAA 240
 QY 1995 GTGTAGGATCTGTAGTACACAGCTGTGATGA 2028
 Db 241 GTGTAGGATCTGTAGTACACAGCTGTGATGA 274

RESULT 68

LOCUS AW641341 553 bp mRNA linear EST 26-APR-2001
 DEFINITION cm06d01.w1 Blackshear/Soares normalized Xenopus egg library
 laevis cDNA clone PBX0105D01 5', mRNA sequence.
 ACCESSION AW641341
 VERSION AW641341.1 GI:7398599
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;

REFERENCE

AUTHORS

Xenopodinae; Xenopus.
 1 (bases 1 to 553)
 Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G.
 Jr., Moore, D.T., Bouffard, G.G., Backstrom-Sternberg, S.M., Touchman
 J.W., Bonaldo, M.F. and Soares, M.B.
 The NIHES Xenopus maternal EST project: interim analysis of the
 first 13,879 ESTs from unfertilized eggs
 Gene 267 (1), 71-87 (2001)
 21211403

TITLE

JOURNAL

MEDLINE

COMMENT

Contact: Perry J. Blackshear
 Office of Clinical Research and Laboratory of Signal Transduction
 National Institute of Environmental Health Sciences
 A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
 USA
 Tel: 919 541-4899
 Fax: 919 541-4571
 Email: black009@niehs.nih.gov
 Clone is available through Research Genetics, Inc., 2130 Memorial
 Parkway, Huntsville, AL 35901
 phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
 cdna@reagen.com
 DNA Sequencing and analyses performed by National Institutes of
 Health Intramural Sequencing Center (NISC).

PCR PRIMERS

FORWARD: TGTAACACGACGCCAGT

BACKWARD: CAGGAACAGCTATGACC

Plate: 0105 row: D column: 01

Seq primer: T7 primer.

Location/Qualifiers

FEATURES

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 /clone="PBX0105D01"
 /clone_lib="Blackshear/Soares normalized Xenopus egg
 library"
 /sex="female"
 /tissue_type="unfertilized egg"
 /cell_type="unfertilized egg"
 /dev_stage="unfertilized egg"
 /lab_host="DH10B"

/note="Vector: p7T3-Pac; Site 1: EcoRI; Site 2: NotI;
 PolyA-selected mRNA was prepared from unfertilized Xenopus
 laevis eggs. The library was constructed in the vector
 p7T3-Pac as described in Bonaldo, M.F., Lennon, G. and
 Soares, M.B. 'Normalization and subtraction: two
 approaches to facilitate gene discovery', Genome Research
 6:793-806, 1996. The first strand synthesis used a
 NotI-dT18 primer; double stranded cDNAs were ligated to
 EcoRI adaptors, digested with NotI, and directionally
 cloned into the NotI and EcoRI-digested p7T3-Pac vector.
 The library contained approximately 7.2 X 10⁵
 recombinants, with average insert sizes of 1-1.5 kb."

BASE COUNT 139 a 155 c 125 g 134 t

ORIGIN

Query Match 13.5%; Score 273; DB 2; Length 553;
 Best Local Similarity 78.4%; Pred. No. 7e-59;
 Matches 327; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
 QY 1 CAAAGGACAAGATAATAAGTACAAATGGTTTCGTTTACATCAGAGGATACAGTTTCATG 60
 Db 33 CAAACAATGATCTTATTTTCAGTTCAAAACGGATCCCTGCATCAGAGGACAGCGTGCACG 92
 QY 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATACAGATACAGTTACCCCTCAA 120
 Db 93 ATAATGACTTTGAGCAGTACCTTCGCGGCGAGTCCCAATCAGAGTAACAGTACCCCTCCA 152
 QY 121 TGAGGACCCCTTACCTGTCCAGCTATTACCGCGGCTCCATTTGGATTTCCTTACTCCCTCA 180
 Db 153 TGACAGACCCCTTATCTATCCAGTTACTACCTCTCTTATTTGGCTTTCCGTATCCCTCA 212
 QY 181 ATGAGGCTCGTGGTCTTACTGACAGGGACCCCTCCGATTTCATACCTCACCTACCGGAC 240


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Db 213 GCGAGCTCCTTGGTCAACTGGTGGGACCCCCCATTCCTTACCTACCCCGTAGGAC 272
QY 241 AGCTCAGTAACGAGACCATCATTTTATGACGATGCTGTTTTGGGCGACCTTGGGGCC 300
Db 273 AGCTCAGCAACGAGATCACCATTTCATGATGATGACGCTTTGGGCGACCTTGGAGCC 332
QY 301 TGGGGAAACATCTATCAGCAGCAGGTTCAATTTTTCCTGAAACCCCTGGTTCTCAG 360
Db 333 TGGGGAATAACATTTATCAACACCGCTTCAACTTCTCCGAGAAACCCAGGCTTTTCTG 392
QY 361 CATGGGGACAGTGGTCTCAAGGTCAGCAGACCCAGAGCTCAGCTCTCCAGCA 417
Db 393 CTTGGGGACAAGTGGCTCCAGGGCAGCAGACCAGAACTCTGCTATGGGGCA 449

RESULT 69
AW420132 639 bp mRNA linear EST 09-FEB-2000
LOCUS fJ8f09.y1 zebrafish gridded kidney Danio rerio cDNA 5' similar to
DEFINITION TR:064526 O64526 YUPB12R.13 PROTEIN. i, mRNA sequence.
ACCESSION AW420132
VERSION AW420132.1 GI:6948064
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio
REFERENCE 1 (bases 1 to 639)
AUTHORS Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@watson.wustl.edu
CDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, Missouri (web address:
www.genomesystems.com) (email contact: info@genomesystems.com) and
Research Genetics, Huntsville, Alabama (web address: www.resgen.com)
) (email contact: info@resgen.com) and
ResourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
www.rzpd.de)
Seq primer: T3 ET from Amersham
High quality sequence stop: 436.
FEATURES
Location/Qualifiers
1..639
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/db_xref="taxon:7955"
/clone_lib="zebrafish gridded kidney"
/sex="mixed"
/tissue_type="kidney pooled from 300 wild type adults"
/lab_host="XLOLR"
/notes="Organ: kidney; Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; Oligo dt cDNA library constructed from mRNA pooled from pooled kidney tissue from 300 adult zebrafish."
BASE COUNT 136 a 194 c 189 g 120 t
ORIGIN
Query Match 13.4%; Score 272.6; DB 2; Length 639;
Best Local Similarity 68.9%; Pred. No. 9.2e-59;
Matches 399; Conservative 0; Mismatches 159; Indels 21; Gaps 1;
QY 421 CCCCCAGCTTTGGTCAACCGCAGTATCAGAGCCCTCAGCAGGCCACCCAGAGCCCGCTGG 480

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Db 61 CCACCCCTCCGAGCCTTACCAGAACCCAGCCCTGCTCTCCCGCCAAACTCGGTGG 120
QY 481 GTTGTCCCAACGCAACAGAAACCGCGCTTTGGGCGAGAGCGGAGGGCTGGCAGCGATAGC 540
Db 121 GTTGTCCCAACGCAACCGCAACCTCGTTATGGTGGAGGAAGCGTGGACAGCAGTGGC 180
QY 541 AACTCTCTGGAACGTCAGCCTTAATTCGTG-----CCCCCAGC 579
Db 181 TCCTCGAGTGGTGGAGGGTCCGCAATGGAGCGGAGGTGGCCACC CGGCTTCCCGCGCC 240
QY 580 GTCGAATCCCAACCGCTCTTGAAAACTGAAGGCTGTCACAGCTACAAACCCGAAAGAG 639
Db 241 ATCGAGTCCCATCCCGCTTTAGAAAGCTGCTGCGGCACACAGCTACAAACCCGAGGAG 300
QY 640 TTTGAGTGAATCTGAAAGCGGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGAC 699
Db 301 TTCGATTGGAACCTGAAAAATGGCCGGGTTCATCATTAAGAGCTACTCTGAGGACGAC 360
QY 700 ATCCACCGCTCCATTAAGTACTCCATCTGGTGTAGCAGACGCGCAGCAGCGCCCTG 759
Db 361 ATCCATCGCTCCATCAAGTACTCCATCTGGTGCAGCAGCGAACATGGAACCAAGCGGCTG 420
QY 760 GACAGCGCTTCCGCTGATGAGCAGCAAGGGCGCGTCTACCTCTTTCAGCGTCAAT 819
Db 421 GATTCGCGTTTCGCGCCATCAACGGCAAGGTCTCTGCTACTGTTTCAGCGTCAAC 480
QY 820 GCGAGTGGGCATTTTGTGGGTGGCGAGATGAAGTCCCGCTGGAGCTACGCGCCACGT 879
Db 481 GCGAGCGACACTTCTGTGGCGTGGCGAGATGCGTTCGCTGTGACTACGCGCCACT 540
QY 880 GCGGGGTCTGCTCTCAGACAAAGTGGAGGGGAAGTTGATGTCCAGTGGATTTTGTGT 939
Db 541 GCGCGTGTGTGGCGCAGGACAAAGTGGAGGGCAATATGATGTGGACTGGCTGTGTGTC 600
QY 940 RAGGATGATCCCAATAACAGCTCCGCGACATCAGGCTG 978
Db 601 AAGAGCGTGGCCCAACAGTCAGCTCAAGCGCATGCGCGCTG 639

RESULT 70
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LOCUS AW168034 Ol-br-ad cDNA Oryzias latipes cDNA clone br1650, mRNA
DEFINITION sequence.
ACCESSION AW168034
VERSION AW168034.1 GI:12590103
KEYWORDS EST.
SOURCE Japanese medaka.
ORGANISM Oryzias latipes
REFERENCE 1 (bases 1 to 740)
AUTHORS Mita, K., Ishikawa, Y. and Yamauchi, M.
JOURNAL Establishment of cDNA database of medaka, Oryzias latipes
COMMENT Unpublished (2001)
Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmिता@nirs.go.jp
method: uni-directional sequence direction: sequenced from T3 primer
(5' -> 3').
FEATURES
Location/Qualifiers
1..740
/organism="Oryzias latipes"
/strain="HNI"
/db_xref="taxon:8090"
/clone_lib="br1650"
/sex="female/male mixed"

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/tissue_type="brain"
/dev_stage="adult"
BASE COUNT      196 a      204 c      167 g      173 t
ORIGIN

Query Match      13.4%; Score 271.4; DB 1; Length 740;
Best Local Similarity 78.2; Pred. No. 1.9e-58;
Matches 326; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 1 CAAAGGACAGATATAAAGTACAAAATGGTTGTTACATCAGAAGGATACAGTTCATG 60
Db 315 CAAAGGACAGATCTAAAGTACAAAATGGATCTCTGCATCAGAGGAGTCTGTCCATG 374

Qy 61 ACAATGACTTTGAGCCCTACCTTACTTGACAGTCAAAATCAGAGTAACAGTTACCCCTCAA 120
Db 375 ATAATGACTTTGAGCCATACCTTACCAGTCAGTCAAGCAGATAAAGCTACCAGTCCA 434

Qy 121 TGAGGACCCCTACTCTCCAGCTATTACCCGCGTCCATTTGGATTTCCTTACTCCCTCA 180
Db 435 TCATGATCCTTACTCTCCAGCTACTATGCTCTCTTATTGGATTTCCGTAACCACTAA 494

Qy 181 ATGAGGCTCCGTGCTACTCGAGGAGACCTCCGATTTCCATACCTCAACCACTACGGAC 240
Db 495 GTGAGGCTCCGTGCTACTGTTGGGATCCACCTATTTCATACCTCACACCTATGGAC 554

Qy 241 AGCTCAGTAACGAGACATCATTTATGACAGATGCTGTTTTTGGGAGCGCTGGGGGCC 300
Db 555 CTTTGAGCAATGGAGACCATCACTTCATCGCGGACACCGTGTGTTGGGAGCGCAGGGGTC 614

Qy 301 TGGGGAACACATCTATCAGACAGGTTCAATTTTTTCCCTGAAAACCCCTGCTTCTCAG 360
Db 615 TGGGAAGCAGCATCTACCGGACAGGTTTAACTTTTTTCCCTGAAAACCCCGCTTCTCTG 674

Qy 361 CATGGGGAACAAGTGGGTCTCAAGTCAGCAGACCGAGCTCAGCCTCTCCCGACA 417
Db 675 CTTGGGGAACAAGTGGGTCTCCAGGCTCAGCAGATCAAAATTCGCGCTATGGTGCA 731

RESULT 71
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LOCUS      0036402.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1568259 3',
DEFINITION      mRNA sequence.
ACCESSION      AA928886
VERSION      AA928886.1 GI:3078243
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgaps-@email.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 514 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 322.
Location/Qualifiers
1. .391
/organism="Homo sapiens"
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FEATURES
source
1. .391
/organism="Danio rerio"

/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; lat strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
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/note="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG);
Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTCTTTTCTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[GTGTGGCCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science) and
kindly donated by Dr. Koichi Kawakami. Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA. "
79 a 115 c 103 g 93 t
BASE COUNT
ORIGIN
Query Match 13.3%; Score 270.6; DB 2; Length 391;
Best Local Similarity 81.0%; Pred. No. 2.6e-58;
Matches 315; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 661 GGGCGTGTTCATCATCAGAGCTACTCTGAGGACGACATCCACGCTCCATTAGTAC 720
DB 390 GGGCGGTGTTCATCATTAAGAGCTACTCTGAGGACGACATCCATCGCTCCATCAAGTAC 331
QY 721 TCCATCTGGTGTAGCAGACGCGCAACAGCGCTTGACAGCGCTTCCGCTCGATC 780
DB 330 TCCATCTGGTGTAGCAGCGACGACATGACAGCGCTGATTCGCTTGTGCGATC 271
QY 781 AGCAGCAAGGGGCCGCTACTCTGCTTTCAGCGTCAATGGGAGTGGCAATTTTGTGG 840
DB 270 AACGGCAAGGTCCTGTCTACTCTGCTTTCAGCGTCAACGCGACGCGACACTTCTGTGG 211
QY 841 GTGGCCGAGATGAAGTCCCGTGGACTAGCGCAGGACGCTGCGGGTCTGGTCTCAGGAC 900
DB 210 GTGGCCGAGATGCGTTCGCTGTGTGACTAGCGCAGGACGCTGCGGTGTGGGCGCAGGAC 151
QY 901 AAGTGAAGGGGAAGTTTGATGTCAGTGGATTTTGTGAAGGATGTACCCCAATAACCAG 960
DB 150 AAGTGAAGGGCAATTTGATGAGTGGCTGCTTGTGTTAAGACGTGCGCCCAACAGTCAG 91
QY 961 CTCGGGCATCAGGCTGGAGATAACGACACAAACCGGTCTCAAACTCCCGGACACC 1020
DB 90 CTCAGGCACATCCGCTGGAGACAATGACACAGCCGCTGACCAACTCGCGTGACACA 31
QY 1021 CAGGAGTGCCCTTAGAAAAAGCCAAAGCA 1049
DB 30 CAGGAGTGCCCTCTGAAAAAGGCCAAAGCA 2
RESULT 73
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LOCUS fil19h06.x1 Sugano Kawakami zebrafish DRA Danio rerio cDNA clone
DEFINITION 2601659 3' similar to TR:064526 O64526 YUP8H12R.13 PROTEIN. ;, mRNA
sequence.
ACCESSION AW116788
VERSION AW116788.1 GI:6083126
KEYWORDS zebrafish.
SOURCE Danio rerio
ORGANISM zebrafish.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 387)
AUTHORS Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra,M., Eddy,S.,
```

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Hillier,L., Clifton,S., Allen,M., Gibbons,M., Jost,S., Kucaba,T.,
Martin,J., Pape,D., Steptoe,M., Underwood,K., Theising,B., Ritter
,E., Bowers,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU Zebrafish EST Project 1999
Unpublished (1999)
Contact: S.L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
Sequencing by: Washington University Genome Sequencing Center
Seq primer: T7 ET from Amersham
High quality sequence stop: 307.
FEATURES
Location/Qualifiers
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/organism="Danio rerio"
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/clone="2601658"
/clone_lib="Sugano Kawakami zebrafish DRA"
/sex="mixed (one male and one female, including
unfertilized eggs)"
/dev_stages="adult"
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/note="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG);
Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTCTTTTCTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[GTGTGGCCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science) and
kindly donated by Dr. Koichi Kawakami. Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA. "
79 a 113 c 102 g 93 t
BASE COUNT
ORIGIN
Query Match 13.3%; Score 269.2; DB 2; Length 387;
Best Local Similarity 81.1%; Pred. No. 5.9e-58;
Matches 313; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 664 CGTGTGTTTCATCATCAGAGCTACTCTGAGGACGACATCCACGCTCCATTAGTACTCC 723
DB 387 CGGGTGTTCATCATTAAGAGCTACTCTGAGGACGACATCCATCGCTCCATCAAGTACTCC 328
QY 724 ATCTGTGTAGCAGACGACGCGCAACAGCGCTTGACAGCGCTTCCGCTGCATGAGC 783
DB 327 ATCTGTGTAGCAGCGACATCGAACAACGCGCTGGATTCTGCGTTTCTGCCATCAAC 268
QY 784 AGCAAGGGGCCGCTCTACCTCTTACCGCTCAATGGGAGTGGGCATTTTGTGGGGTG 843
DB 267 GGCAAAGGTCTCTCTACCTCTGCTTTCAGCGTCAACGCGCAGCGACACTTCTGTGCGGTG 208
QY 844 GCGGAGATGAAGTCCCGCTGAGCTACGCGACAGTGC CGGGGTCTGGTCTCAGGACAG 903
DB 207 GCGGAGATCGTTCGCGCTTGTGACTACGCGCAGTGC CGGGTGTGGGCGCAGGACAAG 148
QY 904 TCGAAGGGGAAGTTTTCATCTCCAGTGGATTTTGTGTTAAGGATGTACCCAATAACCAAGCTC 963
DB 147 TGAAGGGCAAAATTGATGTGAGCTGGCTGTTTGTGTTAAGACGTGCGCCCAACAGTCAAGCTC 88
QY 964 CGGCACATCAGGCTGGAGAATAACGACAAACCGGTCTCAAACTCCCGGGACACCCAG 1023
DB 87 AGGCACATCCGCTGGAGAACAAATGACAAACAGCCCGTGCACCAACTCGCGTGACACAG 28
QY 1024 GAGGTGCCCTTAGAAAAAGCCAAAGCA 1049
DB 27 GAGGTGCCCTCTGAAAAAGGCCAAAGCA 2
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RESULT 74
AA633904/c      652 bp      mRNA      linear      EST 06-MAR-1998
LOCUS
DEFINITION
ac73a10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:868218 3' similar to TR:G849195 G849195 CHROMOSOME IV COSMID
9481. ; mRNA sequence.
ACCESSION
AA633904
VERSION
AA633904.1 GI:2557118
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 652)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin
,J., Moore,B., Scheinberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Insert Length: 1199 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 470.
FEATURES
source
1. .652
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:868218"
/clone_lib="Stratagene lung (#937210)"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/notes="Organ: lung; Vector: pBluescript SK-; Site 1: EcoRI
; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dT, normal lung. Average insert size: 1.0 kb; Uni-ZAP XR
Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'
adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3'"
BASE COUNT 164 a 155 c 130 g 203 t
ORIGIN
Query Match 13.2% Score 266.8; DB 1; Length 652;
Best Local Similarity 74.1% Pred. No. 2.8e-57;
Matches 351; Conservative 0; Mismatches 122; Indels 1; Gaps 1;

Qy 700 ATCCACCGCTCCATTAAAGTACTCCATCTGGTGTAGCAGACGCGCAACAGCGCTG 759
Db 652 ATCCACCGTTCATTAAAGTAAATTTGGTGCAGCAGACGATGTTAACAAGACTG 593

Qy 760 GACAGCGCTTCGCTGTAGCAGACAGAGGGCCGCTTACTGCTCTTCAGCGTCAAT 819
Db 592 GATGCTGCTTATCGTTCCATGAACGGGAAGGCCCGCTTACTTCTTTCAGTGTCAAC 533

Qy 820 GGGAGTGGGCAATTTTGTGGGGTGGCGAGATGAAGTCCCGTGGACTACGGCACCAGT 879
Db 532 GGCAGTGGACACTTCTGTGGCGTGGCAGAAATGAATCTGCTGGGACTACACACATGT 473

Qy 880 GCCGGGGTCTGGTCTCAGGCAAGTGGGAAGGGAAGTTTGAATCTCCAGTGGATTTTGT 939
Db 472 GCAGGTGTGTGTTCCAGGACAAATGGAGGGTCTTTTGTATGTCAGTGGATTTTGTG 413

Qy 940 AAGATGTACCAATAACCACTCCGGCACATACGGCTGGGAGATTAAGCAACAACCG 999

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Db 412 AAGAGCGTTCCCAATAGCCAACTGCGACACATTCGGCTAGAGAACACCGGATTAACCCA 353
Qy 1000 GTCAAAATCCCGGACACCCAGAGAGTGCCTTTAGAAAAAGCCAGCAAGTGTGTA 1059
Db 352 GTGACCACTCTAGGACACTCAGGAAGTGCCTCTCGAAAAAGCTAAGCAGGTGTTGAAA 293
Qy 1060 ATTATCAGTCTTACAGACACAACTCTCATCTTCGACGACTTTTGTCTACTAGGAGAAG 1119
Db 292 ATTATAGCCAGCTACAAAGCACACCACTTCCATTTTGTGACTTCTCACACTATGAGAAA 233
Qy 1120 CGCC-AGAGGAGGAGGTGGTGGCGCAAGGACGCGCAGAGTGGAAACAAACAA 1172
Db 232 CGCCAGAGGAGAGAAAGAGTGTAAAGGAAGCGTCAAGGTCTGGGGAATATA 179

RESULT 75
AA637425
LOCUS
DEFINITION
vu06d08.r1 Soares mammary_gland NDMMG Mus musculus cDNA clone
IMAGE:1179855 5' similar to TR:G849195 G849195 CHROMOSOME IV COSMID
9481. ; mRNA sequence.
ACCESSION
AA637425
VERSION
AA637425.1 GI:2561013
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 476)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisels,S., Kucaba,T., Lacy,M., Le.M., Martin,J., Morris,M.,
Scheinberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:637703
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 467.
FEATURES
source
1. .476
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1179855"
/clone_lib="Soares_mammary_gland_NDMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notes="Organ: mammary gland; Vector: p773D-Pac (Pharmacia
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTTCACCAATCTGAAGTGGAGCGCGCAATGGTGTCTTTTCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonafido."
BASE COUNT 148 a 98 c 121 g 108 t 1 others
ORIGIN

```

Query Match		13.1%; Score 265.2; DB 1; Length 476;
Best Local Similarity		73.7%; Pred. No. 6.5e-57;
Matches 350; Conservative		0; Mismatches 124; Indels 1; Gaps 1;
QY	703	CACCGCTCCATTAGTACTCCATCTGGTGTAGCAGACGCGCAACAAAGCGCTGGAC 762
DB	1	CACCGTTCCATTAGTATTAATATCTGGTGCAGCAGACATGGTAAACAGAGACTGGAT 60
QY	763	AGCGCTTCCGCTGCATGACGAGCGGCGCGTCTACTCTCTCTTCAGCGTCAATGGG 822
DB	61	GCGCCCTATCGTTCATGAATGGAAGGGTCCCGTGTACTTACTTTTCAAGTGTCAACGCG 120
QY	823	AGTGGGCATTTTGTGGGTGCCGAGATGAAGTCCCGTGGACTACGGCAGCAGTGCC 882
DB	121	AGTGACACATCTGTGGAGTTCGAGAGATGAATCTGCTGTGGACTTACACACATGTGA 180
QY	883	GGGCTCTGCTCAGACAAAGTGGAGGGAGTTTGATGTCCAGTGGATTTTGTGAAG 942
DB	181	GGTGTGTGTCCAGACAAATGGAAGGGTCTGTCGATGTGAGATGGATTTTGTGAAG 240
QY	943	GATGTACCAATAACAGCTCCGGCACATCAGGCTGGAGATTAACGACAAACCGGTC 1002
DB	241	GAGTTCCTCCATAGCACTCGCACATCTGCTTAGAGAACACAGAGATAAACAGTG 300
QY	1003	ACAACTCCCGGACACCCAGAGGTGCCCTTAGAAAAAGCAAGCAAGTGTGAAAATT 1062
DB	301	ACCAACTCTAGNGATCCTCAGGAAGTCCCTCTGGAAGAGCTTAAGCAGGTGTGAAAATC 360
QY	1063	ATCAGTCTCTACAGCACACACCTCCATCTTCGACGACTTTGCTCATCAGCAGAGCG 1122
DB	361	ATAGCCAGCTAGAACACACCACTTCCATTTTGTGATGCTTCTCACACTATGAGAAAGC 420
QY	1123	C-AGAGGAGGAGGTGTGGCGCAAGGACGCGAGTGCAGAAACAAACAAATGAG 1176
DB	421	CAAGAGGAGAGAAAGTGTAAAGAGAAAGTCAAGTGTGGGGAATAGAAAG 475
RESULT 76		
AA711690		
LOCUS		AA711690 594 bp mRNA linear EST 24-DEC-1997
DEFINITION		vn58b06.r1 Soares mammary_gland nbmng Mus musculus cDNA clone
IMAGE:1195571 5'		similar to TR:04503 004503 SEQUENCE OF BAC F21M12
FROM ARABIDOPSIS THALIANA CHROMOSOME 1,		COMPLETE SEQUENCE. ;, mRNA
sequence.		
ACCESSION		AA711690
VERSION		AA711690.1 GI:2721608
KEYWORDS		EST.
SOURCE		house mouse.
ORGANISM		Mus musculus
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 594)		Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
		Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
		Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
		Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
		Waterston, R.
TITLE		The WashU-HMI Mouse EST Project
JOURNAL		Unpublished (1996)
COMMENT		Contact: Marra M/Mouse EST Project
		WashU-HMI Mouse EST Project
		Washington University School
		4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
		Tel: 314 286 1800
		Fax: 314 286 1810
		Email: mouseest@watson.wustl.edu
		This clone is available royalty-free through LBNL; contact the
		IMAGE Consortium (info@image.llnl.gov) for further information.
		MGI:642667
		Possible reversed clone: similarity on wrong strand
		Seq primer: -28m3 rev2 ET from Amersham
		High quality sequence stop: 501.
		Location/Qualifiers
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		/db_xref="taxon:10090"
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		/clone_lib="Soares_mammary_gland_nbMNG"
		/sex="male"
		/tissue_type="mammary gland"
		/dev_stage="4 weeks"
		/lab_host="DH10B"
		/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site 1: Not I; Site 2: Eco
		RI; 1st strand cDNA was primed with a Not I - oligo(dT)
		primer [5,
		TGTTACCAATCTGAAGTGGGCGCGCGCAATCGTTTTTTTTTTTTTTTTTTTT
		T 3']; double-stranded cDNA was ligated to Eco RI
		adaptors (Pharmacia), digested with Not I and cloned into
		the Not I and Eco RI sites of the modified pT7T3 vector.
		RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
		constructed and normalized by Bento Soares and M.Fatima
		Bonaldo."
BASE COUNT		153 a 168 c 150 g 123 t
ORIGIN		
Query Match		13.0%; Score 263.6; DB 1; Length 594;
Best Local Similarity		83.8%; Pred. No. 1.8e-56;
Matches 310; Conservative		0; Mismatches 59; Indels 1; Gaps 1;
QY	399	AGCTCAGCTCTCCAGCACAGCCCGCGTGGGT-TGCCCCACGCAACAGAAACCGCGGCTTTGGGCAGA 458
DB	224	AGCTCAACCTCTCCCTGTTTCAGCCCCCACCCTTTGTCAGCCACAGTATCAGAGCCCTCA 283
QY	459	GCAGCCACCCAGACGCGCTGGGT-TGCCCCACGCAACAGAAACCGCGGCTTTGGGCAGA 517
DB	284	GCAGCCACTTCAACCCCGCTGGTGGGCTCTCTCGAAACAGAAATCGACGATTTGGGCAGA 343
QY	518	GGGAGGGGGTGGCGGATGACAACTCTCTCTGGAAAGCTCCAGGCTTAATTTCTGCCCCCA 577
DB	344	GTGGAGGGGGCAACAGTACAGTAACTCTGTTGGAATGCCCAACCTACTTCTGCCCCCA 403
QY	578	GGTTCGAATCCACCCCGCTCTTGAAGAACTGAAGCTGTCTCACAGCTACACCCGAAAG 637
DB	404	GTGTAGAATGCCACCCTGTCTGGAGAACTGAAGCTGCCACAGCTATAACCCCTAAAG 463
QY	638	AGTTTGAAGTGAATCTGAAAAGCGGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGAGC 697
DB	464	AGTTTCGACTGGAACTTAAAGTGGCGGGTGTTCATCATCGAGAGCTATTCTTGAGGAGC 523
QY	698	ACATCCACCGCTCCATTAAAGTACTCCATCTGTTGTAGCAGACGACGCGCAACAGCGCC 757
DB	524	ACATCCACCGCTCCATCAAGTACTCCATCTGTTGTAGTGTAGTGAACAAGGCAACAAGCGCC 583
QY	758	TGCACAGCGC 767
DB	584	TGCACAGCGC 593
RESULT 77		
AA121411		
LOCUS		AA121411 527 bp mRNA linear EST 19-NOV-1996
DEFINITION		zn78e03.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens
		cDNA clone IMAGE:564316 5', mRNA sequence.
ACCESSION		AA121411
VERSION		AA121411.1 GI:1679234
KEYWORDS		EST.
SOURCE		human.
ORGANISM		Homo sapiens
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
		1 (bases 1 to 527)
		Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
		Chlasse, S., Dietrich, N., Dubuque, T., Favellio, A., Gish, W., Hawkins
		, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore

B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)

97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 415.

FEATURES

source
1. .527
/organism="Homo sapiens"
/db_xref="GDB:4596839"
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/clone="IMAGE:564316"
/clone_lib="Stratagene NT2 neuronal precursor 937230"
/tissue_type="neuroepithelial cells"
/dev_stage="Ntera-2 neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/notes="Organ: brain; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Uninduced, exponentially growing neuroepithelial cells (Ntera-2/ci.D1). Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGG 3' -3' adaptor sequence: 5' CTCGAGTGTGTGTGTGTGTGTGT 3' 88 t 4 others
BASE COUNT 123 a 175 c 137 g 88 t 4 others
ORIGIN

Query Match 12.9%; Score 262; DB 1; Length 527;
Best Local Similarity 90.8%; Pred. No. 4.4e-56;
Matches 334; Conservative 0; Mismatches 27; Indels 7; Gaps 5;

QY 387 CAGCAGACCCAGAGCTCAGCTCTCCAGCAGACGCCCGCTTGGCTCAACCGCAGTA 446
DB 133 CAGCCAGCAGGTGGCTCAGCTCTCCAGCAGACGCCCGCTTGGCTCAACCGCAGTA 191
QY 447 TCAGAGCCCTCAGCAGCAGCCAGCCGCTGGTGGTGGCCCGCAGCAGAACGCGGC 506
DB 192 TCAGAGCCCTCAGCAGCAGCCAGCCGCTGGTGGTGGCCCGCAGCAGAACGCGGC 251
QY 507 GTTTGGCAGACCGAGGGGTGGCAGCGATAGCAACTCTCC-TGGAAAGCTCAGCCTA 565
DB 252 GTTTGGCAGACCGAGGGGTGGCAGCGATACAACTCTCTCTTGGAAAGCTCAGCCTA 311
QY 566 ATTCTGCCCCC-AGCGTCGAATCCACCCCGCTCC--TTGAAGAACTGAAGGTGCTCAC 621
DB 312 ATTCTGCCCCCAAGCGTCGAATCCACCCCGCTCTTTGAAAACTGAAAGGTGCTCAC 371
QY 622 AGCTACAACCCGAAAGAG-TTTGAGTGGAACTCTGAAAGGGGGGGCTGTGTTTCATCATCA 680
DB 372 AGCTACAACCCGAAAGAGTTTGGTGGAACTCTGAAAGGGGGGGCTGTGTTTCATCATCA 431
QY 681 GAGCTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCCATCTGGTGTAGCAGAGA 740
DB 432 GAGCTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCCATCTGGTGTAGCAGAGA 491
QY 741 GCACGGCA 748
DB 492 GCACGGAA 499

RESULT 78

BB645804
LOCUS BB645804 695 bp. mRNA linear EST 26-OCT-2001
DEFINITION oblongata Mus musculus cDNA clone B830001A02 5', mRNA sequence.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

BB645804
BB645804.1 GI:16480217
EST.
house mouse.
Mus musculus

REFERENCE AUTHORS

1 (bases 1 to 695)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)

TITLE JOURNAL COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.

FEATURES

Location/Qualifiers
1. .695
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="B830001A02"
/clone_lib="RIKEN full-length enriched, 10 days neonate medulla oblongata"
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/dev_stage="10 days neonate"
/lab_host="DH10B"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second

strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCTCGAGTTAATAATTAATCCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

BASE COUNT 139 a 215 c 189 g 152 t
ORIGIN

Query Match 12.7%; Score 257.8; DB 2; Length 695;
Best Local Similarity 83.9%; Pred. No. 5.5e-55;
Matches 328; Conservative 0; Mismatches 57; Indels 6; Gaps 3;

QY 1 CAAAGGACAGATATAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 60
DB 272 CAAAGGACAGATATAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 331

QY 61 ACAATGACCTTGGAGCCCTACCTTACCTGGACAGTCAATCAGAGTACAGTTACCCCTCAA 120
DB 332 ACAATGACCTTGGAGCCCTACCTTACCTGGACAGTCAATCAGAGTACAGTTACCCCTCGA 391

QY 121 TGAGCAGCCCTACCTGCTCCAGCTATTACCCGCGCTCCATTGGATTTCCTTACTCCCTCA 180
DB 392 TGAGTATCTTACCTGCTCCAGTACTATCCACCATCCATTGGATTTCCTTACTCCCTCA 451

QY 181 ATGAGCTCCGTGCTTACTGCGAGGAGCCCTCCGATTCATACCTACACACCTACCGGAC 240
DB 452 GCGAGGACCATGCTCCACTGCGAGGAGCCCTTCCATCCGATCTTACTACCTATGGAC 511

QY 241 AGCTCAGTACGAGGACCATCATTTTATGACAGTCTGTTTTGGCAGCCTGGGGGCC 300
DB 512 AACTTAATATGAGGACCATCAATTTTATGATGATGCTGTTTTGGGAGCCTGGGGGTC 571

QY 301 T-GGGGACCAACATCTATCAGACA-GGTTCAATTTTTTCCCTGAAACCCCTCGCTTCTC 358
DB 572 TGGGGACCAACATTTATCCACACAGGTTTAAATTTTTTCCCTGAAACCCCGGCATTC 631

QY 359 AGCA----TGGGGACAGTGGGTCTCAAGG 385
DB 632 TTCAGAATGGGGACCAAGTGGGTTTTTAGGG 662

RESULT 79
AA296797
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

RESULT 79
AA296797
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLES
JOURNAL

MEDLINE
COMMENT

96026280
Other ESTs: THC192215
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
source

Location/Qualifiers
1..272
/organism="Homo sapiens"
/db_xref="ATCC (inhost):168367"
/db_xref="taxon:9606"
/clone_lib="Bone VII"
/dev_stage="adult"
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; Site_2: XhoI"

BASE COUNT 92 a 38 c 39 g 99 t 4 others
ORIGIN

Query Match 12.7%; Score 257; DB 1; Length 272;
Best Local Similarity 98.2%; Pred. No. 6.8e-55;
Matches 268; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1355 TAATCTGTAGAGTCACATAAAGGAGTATTTTTTGTGTCAGCTTATCAATCAGACT 1414
DB 1 TAATCTGTAGAGTCACATAAAGGAGTATTTTTTGTGTCAGCTTATCAATCAGACT 59

QY 1415 GATCTAATCTGAAATCTAAGTATCCTTAAACAAAGCATCTATTTGGCAGAAATGTG 1474
DB 60 GATCTAATCTGAAATCTAAGTATCCTTAAACAAAGCATCTATTTGGCAGAAATGTG 119

QY 1475 TTCTTAATTCAGTCATTTGATATTTCTGTGAGACTTCATTTCTCATCCCTTATGCT 1534
DB 120 TTCTTAATTCAGTCATTTGATATTTCTGTGAGACTTCATTTCTCATCCCTTATGCT 179

QY 1535 TTTTACCAACATAGAACCACTAGTCATTTTGTGTCATTTAGATTTCTGATAAATCT 1594
DB 180 TTTNAGCAACATAGAACCACTAGTCATTTTGTGTCATTTAGATTTCTGATAAATCT 239

QY 1595 CTTGAAATCTGAAATCAAAAGGTTAATGATT 1627
DB 240 CTTGAAATCTGAAATCAAAAGGTTAATGATT 272

RESULT 80
BE383024
LOCUS

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT

REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT

REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT

REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LUCM314 row: f column: 08
High quality sequence stop: 629.
Location/Qualifiers
1. .629
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clones="IMAGE:3628807"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 203 a 122 c 152 g 152 t

Query Match 12.6%; Score 255.6; DB 2; Length 629;
Best Local Similarity 74.4%; Pred. No. 1.9e-54; Indels 1; Gaps 1;
Matches 335; Conservative 0; Mismatches 114;
QY 724 ATCTGGTGTAGCACAGACGCGCAACAGCGCTTGGACGCGCTTCCGCTGCATGACG 783
DB 7 ATTTGGTGCACACAGACGCTGTTAAACAGAGACTGGATGCTTATCGTTCCATGAAC 66
QY 784 AGCAAGGGGCGCTTACCTGCTTTCAGCGTCAATGGAGTGGGCATTTTGTGGGTG 843
DB 67 GGGAAAGGCGCGTTTACTTACTTTTTCAGTGTCAACGCGCAGTGACACTTCTGTGGCGTG 126
QY 844 GCCGAGATGAAGTCCCGCGTGGACTACGGCACCAGTGGCGGGTCTGCTCAGGACAA 903
DB 127 GCAGAAATGAATCTGCTGTGGACTACAAACATGTGCAGGTGTGTGCTCCGAGCAAA 186
QY 904 TGGAAAGGGGAAGTTTGATGTCCAGTGGATTTTGTGTAAGGATGTACCCAAATAACCAAGCTC 963
DB 187 TGGAAAGGTGCTTTTGATGTCCAGTGGATTTTGTGAGGAGCTTCCCAATAGCCAACTG 246
QY 964 CGGCACATCAGCTGGAGAAATAAGCAACAAACCGGTCAAACTCCCGGAGCACCCAG 1023
DB 247 CGACACATTCGCTTAGAAGCAACAGAGAAATAACAGTGCACCACTCTAGGGACACTCAG 306
QY 1024 GAGTGCCTTTAGAAAAGCAAGCAAGTGTGAAATTTATCAGTTCTTACAAGCACACA 1083
DB 307 GAAGTGCTCTGGAAAGGCTTAAGCAGGTGTGAAATTTATAGCCAGCTACAAGCACACC 366
QY 1084 ACCTCCATCTTCGACGACTTTTGTCTCACTACGAGAAGCGCC-AGAGGAGGAGGAGGTGTG 1142
DB 367 ACTTCCATTTTGTGATCTTCTCACACTATGAGAAACGCCAAGAGGAGAGAAAGTGT 426
QY 1143 CGAAGGAACGGCAGAGTCGAAACAAACAA 1172
DB 427 AAAAAGGAACGTCAAGTCTGTTGGGAAATAA 456

RESULT 81
AL680804 AL680804 XGC-gastrula Silurana tropicalis cDNA clone TGas070b10 5',
LOCUS mRNA sequence.
DEFINITION
ACCESSION AL680804.1 GI:19537178
VERSION
KEYWORDS western clawed frog.
SOURCE Silurana tropicalis
ORGANISM Eukaryote; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 623)

AUTHORS
TITLE
JOURNAL
COMMENT

Taylor, R., Ashurst, J.L., Croning, M.D.R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2002
Unpublished (2001)
Contact: Taylor R
Sanger Centre
Hinxtion, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TGas070b10.p1CSP6
Sequencing primer: p1CSP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.

FEATURES
source

1. .623
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TGas070b10"
/clone_lib="XGC-gastrula"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XL1-blue"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5' of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."
BASE COUNT 184 a 133 c 153 g 153 t

Query Match 12.2%; Score 246.8; DB 1; Length 623;
Best Local Similarity 73.0%; Pred. No. 3.4e-52;
Matches 317; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 691 GAGGACGACATCCACCGCTCCATTAAAGTACTTCCATCTGGTGTAGCAGACGACGCGCAAC 750
DB 12 GAGATGACATTCACCGCTCCATCAAGTACAAATGTTGGTGTCTACAGAGCATGGTAAC 71
QY 751 AAGCGCTGAGACAGCGCTTCCGCTGCATGAGCAGCAAGGGGCGCGCTTACCTGCTCTTC 810
DB 72 AAGCGCTGAGTGCAGCTTATCGCTCTCTTAATGGCAAGGTCACCTTTACCTGCTTTT 131
QY 811 AGCGTCAATGGGAGTGGGCATTTTGTGGGTGGCCAGATGAAGTCCCGCTGGACTAC 870
DB 132 AGTGTAAATGGTGTAGTGGCCACTTCTGTGGAGTTGACAGAAATGCGCTCAGCAGTAGACTAT 191
QY 871 GGCAACAGTCCCGGGTCTGCTCTCAGGACAAAGTGGAGGGGAAGTTTGTGTCAGTGG 930
DB 192 AATACTTGTGGGAGTTTGGTACAGGACAAATGGAAAGGCGCGCTTGTGTCGCTGG 251
QY 931 ATTTTGTTAAGGATGTACCCAAATAACAGCTCCGGCACATCAGGCTGGAGAAATAACGAC 990
DB 252 CTTTTTGTCAAGGATGTACCTTAATGGACAGTTACGTCACTTCGTCTAGAGAACAAATGAC 311
QY 991 AACAAACGGTCAAACTCCGGGACACCCAGGAGGTGCGCTTAGAANAAGCCAGCAA 1050
DB 312 AACAAACGAGTCCACCAACTCTCCGGGACACCAAGAGGTGCCATTTGGAAAGAGCCGACAG 371
QY 1051 GTGCTGAAAATTATCAGTTCTCAAGCACACACCTCCATCTTCGACGACTTTGTCTCAC 1110
DB 372 GTGCTTCGAAATCATTTGCCAGCTACAGCACACACCTCCATCTTTGATGATTTCTCTCAT 431
QY 1111 TAGCAGAAAGCGCCA 1124
DB 432 TATGAGAAGAGGCA 445

RESULT 82
AW510247/c
LOCUS

DEFINITION
ACCESSION AW510247
VERSION
675 bp mRNA linear EST 03-MAR-2000
fk11c02.x1 zebrafish fin day3 regeneration Denio rerio cDNA 3',
similar to TR:064526 O64526 YU98H12R.13 PROTEIN. ;contains Alu
repetitive element;; mRNA sequence.

AW510247
AW510247.1 GI:7148325

KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio

REFERENCE 1 (bases 1 to 675)
AUTHORS Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.

TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu

CDNA Library Preparation: Raymond Lee. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: misouri@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and ResourceZentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)

Seq primer: T7 ET from Amersham
High quality sequence stop: 218.
Location/Qualifiers
1. 675
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="zebrafish fin day3 regeneration"
/sex="mixed male and female"
/tissue type="3 day fin regenerates"
/lab host="E. coli XL0LR"
/note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; 1st strand cDNA primed with (GA)10ACTAGTCTCGAG(T)18, followed by second strand synthesis, and ligated to 5' adapter (5'-aatcgcgcag-3', 3'-gccgtgtc-5'. cDNA was cloned directionally (EcoRI/XhoI) into Stratagene Zap express lambda phage arms. Mass invivo excision done to obtain inserts in pBK-CMV phagenid."

BASE COUNT 162 a 170 c 164 g 179 t

ORIGIN
Query Match 12.1%; Score 245; DB 2; Length 675;
Best Local Similarity 71.8%; Pred. No. 9.9e-52;
Matches 348; Conservative 0; Mismatches 135; Indels 2; Gaps 2;

QY 667 GTGTTTCATCATCAAGAGCTACTCTGAGGACGACATCCACGGCTCCATTAGTACTCCATC 726
DB 675 GTCTACTTCTCCAAAGAGTACTCTATGGGCGATATCCACGGATCCATTACGGACTATAIT 616

QY 727 TGGTGTAGCAGACGACGCGCCTGGAGCGCCTTCCGCTGCATGACGACG 786
DB 615 TGGTGCAGCGCAGCTCATGTCTCATAGCGGTGGACCCCTGCATTCGGTTCGCTAGCAAC 556

QY 787 AAGGGCCCGTC-TACCTGCTCTTACGCGTCAATGGAGTGGGCATTTTGTGGGGTGGC 845
DB 555 ATAGGGCCACTCGTACTGCTGTTCAGTGTGATGATGCGATGGCCATCTTGTGGCGTGGC 496

QY 846 CGAGATGAAGTCCCCCGTGAAGTACGGCACCAGTCCGGGGTCTGTCTCAGGACAAGTG 905
DB 495 GTAGATGCGCTCGCTGTGGCCTTCAACACTTGTGAGGGCGTGTGGTCGAGGACAAGTG 436

QY 906 GAAGGGGAAGTTGATGTCAGTGGATTTTGTAGGATGTACCCAAATAACGAGCTCG 965
DB 435 GAAGGGTGTGTTGATGTGGCGTGGATCTTTGTCAAGGACGTTTCCCAACAGCCCCACTAAG 376

QY 966 GCACATCAGGCTGGAGATAAGACCAACACCGGTCAAACTCCCGGACACCAGGA 1025
DB 375 GCACATTCGCTTGGAGAAACAATGAGATAAGCGGTAAACCACTCTCGGACACACAGGA 316

QY 1026 GTGCGCTTTAGAAAAAGCAAGCAAGTCTGAAAATATTCAGTTCTCTCAAGCACACAAAC 1085
DB 315 GTTCTCTTAGACAAGGACGCTCAAGTGTGAGATCATCGGAGTTACAGCACACACAC 256

QY 1086 CTCCATCTTTCAGCAGCTTTTGTCTACTACGAGAAGCCCA-GAGGAGGAGGAGGTGGTGG 1144
DB 255 CTCCATTTTTCAGCAGCTTCTCACACTACGAGAAGCGTCAGGAAGAGGAGGAGGTGTA 196

QY 1145 CRAAG 1149
DB 195 AAGG 191

RESULT 83
AW149010/c
LOCUS AW149010 611 bp mRNA linear EST 03-NOV-1999
DEFINITION xf08d09.x1 NCI CGAP Kid8 Homo sapiens CDNA clone IMAGE:2617457 3' similar to TR:O64526 O64526 YUP8H12R.13 PROTEIN. ;, mRNA sequence.
ACCESSION AW149010
VERSION AW149010.1 GI:6196906
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 611)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Possible reversed clone: polyt not found
Seq primer: -40UP from Gibco
High quality sequence stop: 409.
Location/Qualifiers
1. 611
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2617457"
/clone_lib="NCI-CGAP_Kid8"
/tissue type="renal cell tumor"
/lab host="DH10B"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.2 kb. Life Technologies catalog #:
11524-014"

BASE COUNT 145 a 145 c 115 g 206 t

ORIGIN
Query Match 12.1%; Score 244.4; DB 2; Length 611;
Best Local Similarity 73.7%; Pred. No. 1.4e-51;
Matches 311; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 751 AAGCGCTTCAGACAGCGCTTCGCTGCATGACGACGAGGCGCGCTTACCTGCTCTTC 810
DB 611 AGAGACTGGATGCTGCTTATCGTCCATGAACGGGAAGGCCCGCTTACTTCTTTC 552

QY 811 AGCGTCAATGGAGTGGGCATTTTGTGGGGTGGCGAGATGAAGTCCCGCTGGACTAC 870
DB 811 AGCGTCAATGGAGTGGGCATTTTGTGGGGTGGCGAGATGAAGTCCCGCTGGACTAC 870

SOURCE western clawed frog.
ORGANISM *Silurana tropicalis*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; *Silurana*.
1 (bases 1 to 637)
REFERENCE Huckie, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
AUTHORS Sanger Xenopus tropicalis EST project 2001 (10_2001)
TITLE TROPICALIS SEQUENCE ID: TCas009e16.sp6
JOURNAL Unpublished (2001)
COMMENT Contact: Huckie E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropesanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TCas009e16.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.

FEATURES
source
Location/Qualifiers
1..637
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TCas009e16"
/clone_lib="XGC-gastrula"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XL1-blue"
/notes="Vector: PCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dt primed from Sug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into PCS107 with EcoRI at the 5' end and NotI at the 3'
end."

BASE COUNT 165 a 165 c 144 g 163 t

ORIGIN
Query Match 11.8%; Score 239; DB 1; Length 637;
Best Local Similarity 71.5%; Pred. No. 3.3e-50;
Matches 314; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
QY 583 GAATCCCAACCCCGCTTGAAGAACTGAAGGCTGCTACAGCTACACACCGCAAGAGTTT 642
DB 199 GAGCTCACCTGTCTGGAGAAATGGTTCCTCAACACTACATCCNAGACTTT 258
QY 643 GAGTGGAACTGAAAGCGGCGTGTTCATCATCAAGACTACTCTGAGGACGACATC 702
DB 259 GACTTCAGCCTTAAACTTGGTCGGGTGTTCAATGTAAAGAGCTATTGAGGATGACATT 318
QY 703 CACCGCTCCATTAGTACTCCATCTGTTAGCAGACGACGACGACGCTGAC 762
DB 319 CACCGCTCCATCAAGTACAATGTTTGGTGTCTACAGAGCATGGTAACAAGCGCTGGAT 378
QY 763 AGCGCTTCGCTGCATGAGCAGCAAGGGGCCGCTCTACCTGCTCTTCAGCGTCAATGGG 822
DB 379 GCAGCTTATGCTCTCTTAATGGCAAGTCCACTTTACCTGCTTTTAGTGTAAATGGT 438
QY 823 AGTGGGCATTTTGTGGGGTGGCCGAGATGAAGTCCCGCTGGACTACGGCACCAGTGCC 882
DB 439 AGTGGCCACTTCTGTGGAGTTGCAGAAATGCGCTCAGCAGTAGACTATAATCTTGTGGC 998
QY 883 GGGGTCTGGTCTCAGGACAGTGAAGGGGAGTGTGATGTCAGTGGATTTTGTGTAAG 942
DB 499 GGAGTTTGGTTCACAGGACAAATGAAGGGCGCTTTGATGTGCGCTGGCTTTTGTCAAG 558
QY 943 GATGTACCCCAATACAGCTCCGGCAGATCAGGCTGGAGAAATACGACACAAACCGGTC 1002
DB 559 GATGTACTAATGGACAGTTACGTGCATCTCTAGAGAAATGATGAACAGCCAGTC 618
QY 1003 ACAAACTCCGGGACACCC 1021
DB 619 ACCAACTCTCGGACACAC 637
RESULT 88
AW767145

LOCUS AW767145 568 bp mRNA linear EST 16-FEB-2001
DEFINITION da63d11.y1 Harland stage 19-23 *Xenopus laevis* cDNA clone
IMAGE:3199605 5', mRNA sequence.
ACCESSION AW767145
VERSION AW767145.1 GI:7699143
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM *Xenopus laevis*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; *Xenopus*.
1 (bases 1 to 568)
REFERENCE Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
AUTHORS Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person,
B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
Waterston, R. and Wilson, R.
TITLE WashU Xenopus EST project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by R. Harland, PhD (University of California,
Berkeley)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 486.

FEATURES
source
Location/Qualifiers
1..568
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:3199605"
/clone_lib="Harland stage 19-23"
/tissue_type="neurula"
/dev_stage="stage 19-23"
/lab_host="DH10B (phage-resistant)"
/notes="Vector: PCS107 (custom); Site 1: NotI; Site 2: SalI
; cDNA made by oligo-dT priming. Library constructed by
Dr. Francesca Mariani in the laboratory of R. Harland,
Ph.D. (University of California, Berkeley). References:
XBF-2 is a transcriptional repressor that converts
ectoderm into neural tissue. Mariani, FV. Harland, RM.,
Development. 1998 Dec;125(24):5019-31. PMID: 9811586; UI:
99030283; Use of large-scale expression cloning screens in
the *Xenopus laevis* tadpole to identify gene function.
Grammer TC, Liu KJ, Mariani FV, Harland RM., Dev Biol.
2000 Dec 15;228(2):197-210. PMID: 1111324; UI: 20564075;
Note: This is a Xenopus Gene Collection (XGC) library."

BASE COUNT 128 a 196 c 119 g 125 t

ORIGIN
Query Match 11.7%; Score 237.4; DB 2; Length 568;
Best Local Similarity 80.8%; Pred. No. 8.1e-50;
Matches 277; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 1 CAAAAGGACAAGATAATAAAGTACAAATGGTTCGTTTACATCAGAAGTACAGTTTCATG 60
DB 226 CAAAGGACAAGACAGTAAGATTCNAAACGGATCCCTGCATCAGAGGACAGCGTGACG 285
QY 61 ACAATGACTTTGAGCCCTACCTTACTGACAGTCAATCAGAGTAACAGTTACCCCTCAA 120
DB 286 ATAATGACTTTGAGCAGTACCTGTGCGGGCAGTCCAAATCAGAGTAACAGTACCCCTCCA 345
QY 121 TGAGCGNACCCCTACCTGTCCAGCTATTACCGGGCGGTCATTGGATTTCCTTACTCCCTCA 180
DB 346 TGACAGACCCCTTATCTATCATCCAGTTACTACCCCTCTCTTATTTGGCTTTCCGTTATTCCTCA 405

kidney, heart, spleen, ovary, and muscle. The UI-R-E1 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CO) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-A1 and UI-R-E1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Luife Technologies) to generate the UI-R-CO library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)." 125 a 106 g 91 t

BASE COUNT	125 a	89 c	106 g	91 t
ORIGIN				
Query Match	11.5%	Score 233.2;	DB 1;	Length 411;
Best Local Similarity	75.7%	Pred. No. 8.7e-49;		
Matches 289;	Conservative 0;	Mismatches 93;	Indels 0;	Gaps 0;
Qy	743	ACGGCAACAAGCGCTGGACAGCGCTTCCGCTGCATGACGACGAGGGGCCCGTCTACC	802	
Db	9	AAGGTAAACAAGAGACTGGATCGCGCTATCTGTTCCATGAACGGGAAGGTCCTCCGCTACT	68	
Qy	803	TGCTCTTCAGCGCTCAATGGGAGTGGGCATTTTGTGGGGTGGCCGAGATGAAGTCCCCCG	862	
Db	69	TACTTTTCAGTGTCAACGGCAGTGGACACTTCTGTGSGAGTTTGCAGAGATGAATCTGCTG	128	
Qy	863	TGGACTACGGCACCAAGTCCCGGGTCTCGTCTCAGGACAAAGTGGGAAGGGAGTTTGTATG	922	
Db	129	TGGACTACACACATGTCAGGTGTGCTGCCAGACAAATGGGAAGGTCGTTTGTACG	188	
Qy	923	TCCAGTGGATTTTGTTTAAGGATGTACCCAAATAACAGCTCCGGCACATCAGGCTGGAGA	982	
Db	189	TCAGATGGATTTTGTGAAGGACGTTCCCAATAGCCAACTGCGACACATTCGTCTAGAGA	248	
Qy	983	ATACGCAACAACACCGGTCAAAACTCCCGGGACACCCAGGAGTGGCCCTTAGAAAAAG	1042	
Db	249	ACAAAGGAGATAAACCAAGTGAACCAACTTAGGGACACTCAGGAAGTGCTCTGGAAAAAG	308	
Qy	1043	CCAAAGCAAGTGCTGAAAAATTATCAGTTTCTTACAAGCACACAACTTCCATCTTCAGCAGCT	1102	
Db	309	CTAAGCAGGTGTTGAAANAATCATGCCAGCTACACAGCACACCACCTTCCATTTTGTATGACT	368	
Qy	1103	TGTGCTCACTACGGAAGCGCCA	1124	
Db	369	TCTCACACTATGAGAAACGCCA	390	

RESULT 91	
LOCUS	AW276263
DEFINITION	xr08h12.x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:2759591 3' similar to TR:O64526 O64526 YUPH12R.13 PROTEIN.; mRNA sequence.
ACCESSION	AW276263
VERSION	AW276263.1
KEYWORDS	GI:6663293
SOURCE	HUMAN.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1. (bases 1 to 605)
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT	Unpublished (1997) Tumor Gene Index Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange. The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 428.

```

FEATURES
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1. .605
Location/Qualifiers
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:2759591"
/clone_lib="NCI CGAP Lu28"
/tissue_type="two pooled squamous cell carcinomas"
/lab host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site:1: Salt;
Site:2: Notd; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies."
142 a 146 c 122 g 193 t 2 others
BASE COUNT
ORIGIN

```

BASE COUNT	142 a	146 c	122 g	193 t	2 others	
ORIGIN						
Query Match	11.5%	Score 232.8;	DB 2;	Length 605;		
Best Local Similarity	73.0%;	Pred. No. 1.2e-48;				
Matches 311; Conservative	0;	Mismatches 114;	Indels	1;	Gaps	1;
Qy	748	AACAGCGCTGGACACGCGCTTCCGCTGCATGAGCAGCAAGGGGCCGTTACCTGCTC	807			
Db	605	AACAAGAGACTGGATGCTGCTNATCGTTCCATGAACGGGAAGGCCCGTTTACTTACTT	546			
Qy	808	TTACAGCGTCAATCGGAGTGGCGATTTTTTGGGGGTGCCAGATGAAGTCCCCCGTGGAC	867			
Db	545	NTCAGTGTCAACGGCAGTGACACTTCTGTGGCTGGCAAAATGAATCTGCTGTGGAC	486			
Qy	868	TACGGCACCAAGTCCGGGGTCTGGTCTCAGGACAAGTGGGAAGGGGAAGTTTGATGTCCAG	927			
Db	485	TACAACACATGTGCAGGTGTGGTCCAGGACAAATGGAAGGGTCTGTTTGATGTCCAGG	426			
Qy	928	TGAGTTTTTCTTAAGGATGTACCCNATAACACAGCTCCGGCACATCAGGCTGGAGAAATAC	987			
Db	425	TGAGTTTTTGTGAAGGACGTTTCCCAATAGCCAACTGGGACACATTCGCCCTAGAGAACAC	366			
Qy	988	GACAACAAACCGGTCACAAACTCCCGGGACACCCAGGAGTGCCCTTAGAAAAAGCCAAAG	1047			
Db	365	GAGATAAACCAAGTGACCAACTCTAGGGACACTCAGGAAGTGCCCTCTGGAAAGGCTTAAG	306			
Qy	1048	CAAGTGTCTGAAATATTACAGTTCCTCAAGCACACAACTCCATCTTCGACGACTTTGCT	1107			
Db	305	CAGGTGTGTGAAATATTAGCCAGCTCAAGCACACCACTTCCATCTTTGATGACTTCTCA	246			
Qy	1108	CATTACGAGAAGGCCCC-AGAGGAGGAGGAGGTGGTGGCGCAAGGAAACGGCAGAGTCGAAAC	1166			
Db	245	CACTATGAGCCACGCCNAGAGGAAACAGAAAGTGTAAAAAGGAAAGCTCAAGGTCTGGG	186			
Qy	1167	AAACAA	1172			
Db	185	AAATAA	180			

RESULT 92	
BB625167	
LOCUS	BB625167 663 bp mRNA linear EST 26-OCT-2001
DEFINITION	BB625167 RIKEN full-length enriched, adult male Cecum Mus musculus
ACCESSION	CDNA clone 9130022A11.5, mRNA sequence.
VERSION	BB625167
KEYWORDS	BB625167.1 GI:16463485
SOURCE	EST.
ORGANISM	house mouse.
	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


```
source          1. .688
/organism="Ciona intestinalis"
/db xref="taxon:7719"
/clone="rcieg28n18"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
/tissue_type="whole animal"
/dev_stage="egg"
/notes="vector: pbluescript SK"
BASE COUNT      174 a  149 c  135 g   230 t
ORIGIN

Query Match      11.4%; Score 231; DB 2; Length 688;
Best Local Similarity 63.3%; Pred. No. 3.6e-48;
Matches 354; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 595 GTCCTTGAACAACTGAAGCTGCTCACAGCTACACCCGGAAGAGTTTGAGTGAATCTG 654
      |||||
Db 562 GTGTGGGAAATTAAGCTGAAATGACTACACCCCAACCGTTGACCATCGAGCTT 503
      |||||

QY 655 AAAAGCGGCGTGTTCATCATCAAGAGTACTCTGAGGACGACATCCACCGTCCATT 714
      |||||
Db 502 CGGAATGCAAGATTTTGTAAATTAATTCGATTCCTGAAGATGATATTCATCGTTCTATC 443
      |||||

QY 715 AAGTACTCCATCTGCTGACAGACGACCGCAACAGCCCTGACAGCGCTTCGCG 774
      |||||
Db 442 AATATCAACATTTGGTCTCCACTGACCATGGCAACAAACGATTGGATGCGAGCGTTTCGT 383
      |||||

QY 775 TGCATGACGACGAAGGGCGCTCTACTGCTCTTTCAGCGTCAATGGAGTGGGCATTTT 834
      |||||
Db 382 GAACAGCAAGCAAGCGCGTATTTTACTCTACTCTGTAAAGCGTTCTGGTCAATTC 323
      |||||

QY 835 TGTGGGTGGCGAGATGAAGTCCCCCGTGGACTACGCGACCACTGCGGGGTCTGGTCT 894
      |||||
Db 322 TGTGGCGTTCAGAAATGCTCACTCAGATTGACTACAGCAAGCGTGTGGTGTGGCT 263
      |||||

QY 895 CAGCAAGTGGAGGGAGTTTGATGTCAGTGGATTTTGTAAAGGATGACCCCAAT 954
      |||||
Db 262 CAGGATAGTGAAGGAAGTTCAGGTGAATGGATTTATGGAAGGAGCTTCCTTAAC 203
      |||||

QY 955 AACGAGCTCCGGCAGCATCAGCGCTGGAGAAATACGCAACAAACCGGTCAACAACTCCCGG 1014
      |||||
Db 202 AGCCAGCTTCGTATATTCGCTTGAATAATAGTAATAAACCGGTGACAACTCAGT 143
      |||||

QY 1015 GACACGAGAGTGGCCCTTAGAAAAAGCCAAAGCAAGTGTGAAAAATATCAGTTCCTAC 1074
      |||||
Db 142 GACACTCAGGAGTTCCTGCGAGAAAGGAAGACAAAGTCTTAAAAATCATTAGTAGCTAT 83
      |||||

QY 1075 AAGCACACACCTCCATCTTCGACGACTTTGCTCACTACGAGAGCGCCAGAGGAGG 1134
      |||||
Db 82 AAACATCAACAAAGTATATTGTGATGACTTTTCACATTACGAAACGCCCTCAAGGGGAAG 23
      |||||

QY 1135 AGGTGTCGCGCAAGGAACG 1153
      |||||
Db 22 AAGTCTTCGTCAAAACG 4
      |||||

RESULT 94
AW148417
LOCUS      312 bp mRNA linear EST 03-NOV-1999
DEFINITION xfl2h04.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2617879 3',
            mRNA sequence.
ACCESSION  AW148417
VERSION     AW148417.1 GI:6196313
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 312)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL    Unpublished (1997)
```

```
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
FEATURES
            Location/Qualifiers
            1. .312
            /organism="Homo sapiens"
            /db xref="taxon:9606"
            /clone="IMAGE:2617879"
            /clone_lib="NCI_CGAP_Kid8"
            /tissue_type="renal cell tumor"
            /lab_host="DH10B"
            /note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: SalI;
            Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 1.2 kb. Life Technologies catalog #:
            11524-014"
BASE COUNT      95 a   46 c   42 g   127 t   2 others
ORIGIN

Query Match      11.4%; Score 230.6; DB 2; Length 312;
Best Local Similarity 92.3%; Pred. No. 3.7e-48;
Matches 288; Conservative 0; Mismatches 15; Indels 9; Gaps 4;

QY 1413 CTGATCTAATGTGAATGTAAGTATCTTTAAACAAAGCATCTATTTGCGAGAAATTG 1472
      |||||
Db 1 CTGATCTAATGTGAATGTAAGTATCTTTAAACAAAGCATCTATTTGCGAGAAATTG 60
      |||||

QY 1473 TGTCTTAATTCAGTCATTTGATATCTCTGAGACTTCATATTTCTCATCCCTTTATTG 1532
      |||||
Db 61 TGTCTTAATTCAGTCATTTGATATCTCTGAGACTTCATATTTCTCATCCCTTTATTG 120
      |||||

QY 1533 CTTTTAGCAACATAGAAACCATGAGTCATTTTGTCAATTTAGAGTATTTCTGATAAAAT 1592
      |||||
Db 121 CTTTTAGCAACATAGAAACCATGAGTCATTTTGTCAATTTAGAGTATTTCTGATAAAAT 180
      |||||

QY 1593 CTCTGAAAATACGAAATCAAAAGGTTAATGATTTT-TTGTTCATTCGTG-ATTGTGCAT 1650
      |||||
Db 181 CTCTGAAAATACGAAATCAAAAGGTTAATGATTTT-TTGTTCATTCGTG-ATTGTGCAT 240
      |||||

QY 1651 TTATTATTA-----TCGTGTTATCGGTCTAAAGTCTAATTTTACCCA-TTTCATTTTCTGTC 1703
      |||||
Db 241 TTATTATTAATCTGTTATTCGGTCTTTAAAGTGCCTTAATTTTACCCATTTTGATTTTCTGTC 300
      |||||

QY 1704 TAGACAGATAAC 1715
      |||||
Db 301 TAGACAGATAAC 312
      |||||

RESULT 95
AJ396676
LOCUS      674 bp mRNA linear EST 25-JAN-2001
DEFINITION AJ396676 dkfz426 Gallus gallus cDNA clone 27f9r1, mRNA sequence.
ACCESSION  AJ396676
VERSION     AJ396676.1 GI:128853
KEYWORDS   EST.
SOURCE     chicken.
ORGANISM   Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            1 (bases 1 to 674)
AUTHORS   Abdulkhmanov, I., Lodygin, D., Geroth, P., Arakawa, H., Law, A., Plachy
            J., Korn, B. and Buerstedde, J.M.
            A large database of chicken bursal ESTs as a resource for the
            analysis of vertebrate gene function
            Genome Res. 10 (12), 2062-2069 (2000)
JOURNAL
```


MEDLINE 20568495
COMMENT Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institut
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
FEATURES Location/Qualifiers
source 1..674
/organism="Gallus gallus"
/strain="CB"
/db_xref="taxon:9031"
/clone="27f9r1"
/clone_lib="dkf426"
/tissue_type="Bursa of Fabricius"
/cell_type="Bursal lymphocyte"
/dev_stage="2-3 weeks old"
BASE COUNT 207 a 138 c 138 g 190 t 1 others
ORIGIN

Query Match 11.2%; Score 226.6; DB 1; Length 674;
Best Local Similarity 75.6%; Pred. NO. 4.8e-47;
Matches 294; Conservative 0; Mismatches 94; Indels 1; Gaps 1;
QY 785 GCAAGGGCCGCTACCTGCTCTCAGCGTCAATGGAGTGGGCAATTTTGTGGGTG 844
Db 2 GAAAAGGCCCGCTCTATTACTCTTCAGTGTGAATGGCAGTGACACACTTTTGTGGAGTGG 61
QY 845 CCAGATGAAGTCCCGCTGGACTACGGCACCACTGCGGGGTCTGCTCTCAGGACAAAGT 904
Db 62 CTGAGATGAAGTCTGTGTGGACTACATGCATATGCTGCGCTCTGCTCAGGATAAGT 121
QY 905 GGAAGGGGAAGTTGATGTCACGATGATTTTGTAAAGGATGACCAATPAACCACTCC 964
Db 122 GGAAGGGCAAGTTGATGTCAAATGGATCTTTGTCAAAGACGTTCCCAATAACCACTGC 181
QY 965 GGCACATCAGCTGGAGATAACGACACAAACCGGTCAAACTCCCGGGACCCAGG 1024
Db 182 GGCATATTGCTTTGGAACAAATGACAAACAAACCGATTACCAATTGAGGGGACACTCAAG 241
QY 1025 AGGTGCCCTTAGAAAAGCAAGCAAGTGTGAAATTTATCAGTTCTTACAAGCACACAA 1084
Db 242 AAGTACCCCTAGAAAAGCCAGCAAGTGTAAATTAATGCTACTTTTCAAGCATACCA 301
QY 1085 CTTCCATCTTCGACGACTTTGCTCCTACAGAGAGCG-CCAGAGGAGGAGGAGTGGTGC 1143
Db 302 CTTCAATCTTTGATGACTTTTGCACTTTATGAAAGCGTCAAGAAGAGGAGGAGCCATGC 361
QY 1144 GCAAGGACGGCAGAGTCGAAACAAACAA 1172
Db 362 GTAGGGAGAGGAATAGAAACAAACAAATAA 390

RESULT 96
AA352050 236 bp mRNA linear EST 21-APR-1997
LOCUS EST59985 Activated T-cells XX Homo sapiens cDNA 5' end, mRNA
DEFINITION sequence.
ACCESSION AA352050
VERSION AA352050.1 GI:2004370
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 236)
AUTHORS Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter,J.C.
TITLE Rapid cDNA sequencing (expressed sequence tags) from a
directionally cloned human infant brain cDNA library
JOURNAL Nat. Genet. 4, 373-380 (1993)
MEDLINE 94004965
COMMENT Other_ESTs: THC192215
Contact: Kerlavage, AR
Bioinformatics

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1..236
/organism="Homo sapiens"
/db_xref="ATCC (inhost):152236"
/db_xref="taxon:9606"
/clone_lib="Activated T-cells XX"
/cell_type="T-lymphocyte"
/dev_stage="adult"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 54 a 56 c 71 g 49 t 6 others
ORIGIN

Query Match 11.1%; Score 236; DB 1; Length 236;
Best Local Similarity 97.4%; Pred. NO. 5.1e-47;
Matches 226; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 784 AGCAAGGGCCGCTACCTGCTCTTACGCGTCAATGGAGTGGGCAATTTTGTGGGTG 843
Db 1 AGCAAGGGCCGCTACCTGCTCTTACGCGTCAATGGAGTGGGCAATTTTGTGGGTG 60
QY 844 GCGGAGATGAATGCCCGCTGGACTACGGCACAGTGCAGGGGTCTGGTCTCAGGCAAG 903
Db 61 GCGGAGATGAATGCCCGCTGGACTACGGCACAGTGCAGGGGTCTGGTCTCAGGCAAG 120
QY 904 TCGAAGGGGAAGTTGATGTCAGTCCAGTGGATTTTGTAAAGGATGACCAATACCAAGCTC 963
Db 121 TGAAGGGGAAGTTGATGTCAGTGGATTTTGTAAAGGATGACCAATACCAAGCTC 180
QY 964 CGGCACATCAGGTGGAGAAATACGACAAACCGGTCAAACTCCCGGG 1015
Db 181 CGNCACATCAGGTGGAGAAATACGACAAACCGGTCAAACTCCCGGG 232

RESULT 97
BE457388/c 601 bp mRNA linear EST 26-JUL-2000
LOCUS us89b05.xl Soares mammary_gland WMLMG Mus musculus cDNA clone
DEFINITION IMAGE:3325521 3' similar to TR:064526 064526 YUP8H12R.13 PROTEIN.
; mRNA sequence.
ACCESSION BE457388
VERSION BE457388.1 GI:9479474
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 601)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Other_ESTs: us89b05.y1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1069685
High quality sequence stop: 450.
FEATURES Location/Qualifiers
source 1..601
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3325521"

```
/clone_lib="Soares_mammary_gland_NMLMG"
```

```
/sex="Female (lactating)"
```

```
/tissue_type="mammary gland"
```

```
/lab_host="DH10B"
```

```
/note="Vector: p7T3D-Pac (Pharmacia). with a modified  
polylinker; 1st strand cDNA was prepared from mammary  
gland tissue from a lactating female, and was then primed  
with a Not I - oligo(dT) primer. Double-stranded cDNA was  
ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the  
modified p7T3 vector. Library is normalized. Library  
was constructed by Bento Soares and M. Fatima Bonaldo."
```

```
BASE COUNT      146 a  146 c  119 g  190 t
ORIGIN
```

```
Query Match      11.1%; Score 225.2; DB 2; Length 601;  
Best Local Similarity 73.3%; Pred. No. 1.1e-46;  
Matches 315; Conservative 0; Mismatches 113; Indels 2; Gaps 2;
```

```
Qy 750 CAAGCGCTGACAGCGCTTCCGCTGCATGAGCAGCAAGGGCCCGTCTACCTGCTTT 809
```

```
Db 601 CAAGAGACTGGATCGCGCTATCG-TCCATGAATGGGAAGGTCCTCGTACTTTT 543
```

```
Qy 810 CAGCGTCAATGGGAGTGGCATTTTGTGGGGTGGCCGAGATGAATCCCGTGGACTA 869
```

```
Db 542 CAGTGTCAACGGCAGTGGACACTTCTGTGGAGTTGCAGAGATGAATCTGCTGGACTA 483
```

```
Qy 870 CGGCACAGTCCCGGGTCTGGTCTCAGGACAAAGTGGGAAGGGAAGTTGATGCCAGTG 929
```

```
Db 482 CAACACATGTGCAGGTGTGGTCCAGGACAAATGGNAGGGTGGTTTCGATGTCCAGATG 423
```

```
Qy 930 GATTTTGTAAAGATGTACCCAAATACCAAGTCCCGCACATCAGGCTGGAGATAACGA 989
```

```
Db 422 GATTTTGTGAAGGACGTTCCCAATAGCCAACTCGACACATTCGTCTAGAGAACAGCA 363
```

```
Qy 990 CAACAAACCGGTCAAACTCCCGGGACACCCAGAGGTGCGCTTAGAAAAGCCAGCA 1049
```

```
Db 362 GAATAAACCAAGTGAACCACTTAGGGGACACTCAGGAAGTGCCTTGAAAAGAGCTAAGCA 303
```

```
Qy 1050 AGTCTGAAAATATCAGTTCTCTACAGCACACAACTCCATCTTCGACGACTTTTGCTCA 1109
```

```
Db 302 GGTGTTGAAAATCATAGCCACTACAGCACACCACTTCCATTTTGTATGACTTCTACA 243
```

```
Qy 1110 CTACGAGAAGCCGC-AGAGGAGGAGGAGTGTGCGCAAGGAACGGCAGAGTCGAAAACAA 1168
```

```
Db 242 CTATGAGAAACGCCAAGAGGAAGAAAGTGTAAAAAGCAAGCTCAAGTCTGTGGAA 183
```

```
Qy 1169 ACATGAGGG 1178
```

```
Db 182 ATAGAAAGCG 173
```

```
RESULT 98  
AW535358/c  
LOCUS  
DEFINITION      597 bp mRNA linear EST 06-MAR-2000  
UI-R-BS0-aoe-c-04-0-UI.s1 UI-R-BS0 Rattus norvegicus cDNA clone  
UI-R-BS0-aoe-c-04-0-UI 3', mRNA sequence.
```

```
ACCESSION      AW535358  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Norway rat.  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.
```

```
REFERENCE  
1 (bases 1 to 597)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
AUTHORS  
TITLE  
Normalization and subtraction: two approaches to facilitate gene  
discovery
```

```
JOURNAL  
MEDLINE  
COMMENT  
Genome Res. 6 (9), 791-806 (1996)  
97044477
```

```
CONTACT: Soares, MB  
PROGRAM for Rat Gene Discovery and Mapping
```

```
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msoares@blue.weeg.uiowa.edu  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. The sequence tag present in the cDNA between the NotI site  
and the oligo-dT track served to verify it as a clone from the  
non-normalized ovary library cDNA Library Preparation: M.B. Soares  
Lab Clone distribution: clones will be available through Research  
Genetics (www.resgen.com)  
Seq primer: M13 Forward  
POLYA=Yes.
```

```
FEATURES  
Location/Qualifiers  
1..597  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/db_xref="taxon:10116"  
/clone_lib="UI-R-BS0-aoe-c-04-0-UI"  
/dev_stage="embryonic 13 dpc"  
/lab_host="DH10B (Life Technologies)"  
/notes="Vector: p7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BS0  
library is derived from 13 dpc whole embryo tissue. For a  
detailed description of the library from which this clone  
was derived, please visit our web site at  
rategen.eng.uiowa.edu.  
TAG LIB=UI-R-BS0  
TAG TISSUE=ovary  
TAG SEQ=TCAC"
```

```
BASE COUNT      141 a  114 g  200 t
```

```
ORIGIN
```

```
Query Match      11.1%; Score 224.8; DB 2; Length 597;  
Best Local Similarity 73.5%; Pred. No. 1.3e-46;  
Matches 300; Conservative 0; Mismatches 107; Indels 1; Gaps 1;
```

```
Qy 772 CGCTGCATGACGACGAGGCGGCTCTACTGCTCTTCAGCGTCAATGGAGTGGGCAT 831
```

```
Db 596 CGTTCATGAACGGGAAGGGTCCGGTACTTACTTTTCAGTTTCAACGGCAGTGGACAC 537
```

```
Qy 832 TTTTGTGGCGTGGCCGAGATGAAGTCCCGTGGACTACGGCACAGTGCCTGGGCTCTGG 891
```

```
Db 536 TTCTGTGGAGTTGCAGAGATGAATCTGCTGTGGACTACACACATGTGCAGGTGTGG 477
```

```
Qy 892 TCTCAGGACAAAGTGGGAAGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGGATGTACCC 951
```

```
Db 476 TCCAGGACAAATGGGAAGGGTGGTTTTCAGCTCAGATGGATTTTGTGAAGGACGTTCCC 417
```

```
Qy 952 AATAACAGCTCCGGCAGCATCAGCTGGAGATAACGACAAACACCGGTACAACTCC 1011
```

```
Db 416 ATAGCCAACTGGGACACATTCGCTTAGAAGAACACGAGAATAAACCACTGACCACTCT 357
```

```
Qy 1012 CGGACACACCAGAGGTGCCCTTAGAAAAAGCAAGCAAGTGCCTGAAAAATATCAGTTCC 1071
```

```
Db 356 AGGACACTCAGGAAGTGCCTCTGAAAAAGCTTAAGCAGGTGTGAAAAATCATAGCCAGC 297
```

```
Qy 1072 TACAAGCACAAACCTCCATCTTCGACGACTTTGCTCCTACACGAGAACGCC-AGAGGAG 1130
```

```
Db 296 TACAAGCACACCACTTCCATTTTGTATGACTTCTCAGCTATGAGAAACGCCAAGAGGAA 237
```

```
Qy 1131 GAGGAGTGTGGCAGGAACCGCAGAGTCGAAACAAACCAATGAGGG 1178
```

```
Db 236 GAAGAAAGTGTAAAAAGGAACGTCAGGCGCTGGGGAATATAAAGCG 189
```

```
RESULT 99
```

```
AW075266/c
```

```
LOCUS
```

```
DEFINITION      232 bp mRNA linear EST 13-OCT-1999  
wz96e04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:256686 3',
```

mrna sequence.
ACCESSION AW075266
VERSION AW075266.1 GI:6030264
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 232)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 222.

FEATURES
Location/Qualifiers
1..232
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:256686"
/clone_lib="NCI CGAP Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="PH108"
/note="Organ: brain; Vector: pRT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAATGCGAGCGCGATAGGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 91 a 51 c 41 g 49 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.6e-46;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 232 CAATGAGGGGAACCACTTTCTTACATGTTCTAACGTTTTCACCTTTGAAACAGTTTAAAA 173
QY 1230 CAGCTGTGCTTGTGTCAGCTCAGCTGTGTCGTCGCGGGGGTTCAGTGTTCATCTTT 1289
DB 172 CAGCTGTGCTTGTGTCAGCTCAGCTGTGTCGTCGCGGGGGTTCAGTGTTCATCTTT 113
QY 1290 GCCTTTCTTGTGTTGTTTTCGCCAGATGATCTGCATTTATTTGATCTTTTCTATG 1349
DB 112 GCCTTTCTTGTGTTGTTTTCGCCAGATGATCTGCATTTATTTGATCTTTTCTATG 53
QY 1350 TATTATAATCCTGTAGAGTCACTAATAAGAGGATTTTTTTT 1393
DB 52 TATTATAATCCTGTAGAGTCACTAATAAGAGGATTTTTTTT 9

RESULT 100
AW03320
LOCUS
DEFINITION UI-HF-BN0-akx-d-02-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
IMAGE:3078578 5', mRNA sequence.

mrna sequence.
ACCESSION AW503320
VERSION AW503320.1 GI:7118597
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 496)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
Location/Qualifiers
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/tissue_type="lymph"
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/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pRT73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 170 a 87 c 109 g 130 t
ORIGIN
Query Match 11.0%; Score 223.4; DB 2; Length 496;
Best Local Similarity 74.3%; Pred. No. 2.9e-46;
Matches 295; Conservative 0; Mismatches 101; Indels 1; Gaps 1;
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DB 1 CACGAGGGGGAAGGCCCACTCTATTACTCTTCAGTGTGAATGGCAGTGGACATTTTGG 60
QY 837 TGGGTTGGCCGAGATGAAGTCCCCCGTGGACTACGGCACAGTGC CGGGGTCTGTCTCA 896
DB 61 TGGAGTGGCTGAAATGAAGTCTGTTGTGGACTATAATGCGTATGCTGTGCTGTCTCA 120
QY 897 GCACAGTGGAGGGGAAGTTTGATGTCAGTCCAGTGGATTTTGTAGGATGATCCCAATAA 956
DB 121 GGATAGTGGAGGGGCAAAATTTGAAGTTAAATGGATCTTTTGCAAGATGTTCCCAATAA 180
QY 957 CCAGCTCCGCGCATCAGGCTGGAGAAATACGACAAACCGGTCCAAACTCCCGGGA 1016
DB 181 CCAATTACGGCATATTCGCTTAGAANAATATGACAAACCGGTACCAATTCAGGGA 240
QY 1017 CACCCAGGAGGTGCCCTTAGAAAAAGCCAAAGAGTGTGAAAAATATCAGTTCTCTACAA 1076
DB 241 CACTCAAGAGGTACCCCTAGAAAAAGCTAAGCAAGTCTTAAAAATAATTTGCTACTTTCAA 300
QY 1077 GCACACAACCTCATTCTCGACGACTTTGCTCACTACGAGAGCG-CCAGAGGAGGAGGA 1135
DB 301 GCATACCACTCAATCTTTTGATGACTTTTCACATTATGAAGACCGTCAAGAGAGGAGGA 360
QY 1136 GTGTGTGCGCAAGGACGCGCAGAGTCGAAACAAACAA 1172
DB 361 AGCCATGCGGTAGGAGAGAAATAGAAAAACAACATAA 397

Search completed: March 24, 2003, 01:32:06
Job time : 1248 secs

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using ew model

Run on: March 23, 2003, 23:43:46 ; Search time 3338 Seconds
(without alignments)
9839.559 Million cell updates/sec

Title: US-09-877-633-2

Perfect score: 2028

Sequence: 1 caaaaggacaagataataaa.....agtaacagacagtgtgatgga 2028

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 350 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	725.8	35.8	889	14	BQ682082 AGENCOURT
3	701.4	34.6	928	14	BQ421505 AGENCOURT
4	674.6	33.3	1109	12	BE894361 AGENCOURT
5	650.8	32.1	852	12	BE892982 AGENCOURT
6	648.8	32.0	1014	9	AV079675 AGENCOURT

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C	9	628.8	31.0	684	10	AW01012 wr91e06.x
C	10	626.6	30.9	932	10	AV726565 AV726565
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C	12	615.2	30.3	633	14	BM685329 UI-R-C10-
C	13	601.8	29.7	664	10	BE646471 7e87d05.x
C	14	594.6	29.3	689	13	BE911605 602812729
C	15	583.2	28.8	600	10	AW387914 MR4-ST011
C	16	581.8	28.7	808	12	BE892829 601433961
C	17	580.4	28.6	736	13	BI091481 602858960
C	18	571	28.2	669	10	AW964022 EST376095
C	19	555	27.4	582	13	BI262492 602353767
C	20	553.4	27.3	929	12	BQ249197 602361623
C	21	551	27.2	563	10	AW387761 MR4-ST011
C	22	545.6	26.9	893	12	BG216572 RST36264
C	23	542.8	26.8	688	13	BM014798 603640668
C	24	519.2	25.6	837	10	BE542593 601063983
C	25	519	25.6	921	9	AL562740
C	26	512	25.2	598	14	BM931439 UI-E-EJ1-
C	27	506.2	25.0	886	12	BG828010 602752056
C	28	503.6	24.8	659	10	AW387819 MR4-ST011
C	29	502.6	24.8	530	12	BP915645 IL3-UT011
C	30	483.6	23.8	551	10	AW387869 MR4-ST011
C	31	483.6	23.8	688	9	AJ449334 AJ449334
C	32	480.6	23.7	499	10	AW387916 MR4-ST011
C	33	480.4	23.7	538	17	AQ564196 HS 5363.A
C	34	476.4	23.5	964	13	BI739961 603361310
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C	36	472	23.3	1002	14	BQ25658 AGENCOURT
C	37	466.8	23.0	584	10	AW387858
C	38	456.8	22.5	460	9	AA976117 ON33b10.s
C	39	450	22.2	778	9	AL580786
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C	42	442.4	21.8	614	9	AI536382 ma97f06.y
C	43	439.4	21.4	902	14	BQ421488 AGENCOURT
C	44	434.4	21.4	977	13	BM556661 AGENCOURT
C	45	431	21.3	435	14	BM745209 K-EST0019
C	46	430.8	21.2	623	13	BI224711 602949342
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C	48	424.4	20.9	687	13	BQ44639 BJ044639
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82	342.2	16.9	706	13	BQ64834	BQ64834 AGENCOURT	155	271.4	13.4	727	12	BQ018594
83	340.5	16.8	883	14	BQ223830	BQ223830 AGENCOURT	156	271.4	13.4	740	9	AU168034
84	339	16.7	739	17	BH353078	BH353078 CH230-163	157	271	13.4	791	9	AA928886
85	338	16.7	917	9	AL515909	AL515909 AL515909	C 158	270.6	13.3	391	10	AW116778
86	336.8	16.6	355	9	AA460050	AA460050 ZK66C02.r	159	270.4	13.3	741	12	BF983198
87	336.2	16.6	937	14	BQ899696	BQ899696 AGENCOURT	160	269.8	13.3	666	13	B1261821
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94	333	16.4	694	14	BM772351	BM772351 K-EST0056	167	265.4	13.1	571	14	BQ0520373
95	332	16.4	505	14	BM748094	BM748094 K-EST0022	168	265.2	13.1	476	9	AA637425
96	327	16.1	341	9	AA361068	AA361068 EST70314	169	264.6	13.0	885	12	BG245774
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98	324.8	16.0	411	14	N95559	N95559 YF60d10.r1	C 171	263.4	13.0	707	14	BM973093
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102	321	15.8	713	14	BQ773021	BQ773021 UI-H-FEO-	C 175	259.4	12.8	567	13	BM391094
103	320.6	15.8	338	9	AA377640	AA377640 EST90244	C 176	259.2	12.8	678	12	BF733041
104	319.4	15.7	521	10	AM465438	AM465438 BF230019A	C 177	258.4	12.7	635	13	BM240020
105	317.2	15.6	819	12	BE897197	BE897197 601439762	178	257.8	12.7	695	10	BB645804
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108	315.8	15.6	457	12	BG804877	BG804877 0273-49 M	C 181	257	12.7	592	13	BJ100170
109	313.4	15.5	524	13	BM194314	BM194314 TCAAP1Q95	182	255.6	12.6	449	14	W05553
110	313	15.4	373	14	W14779	W14779 ma97f06.r1	183	255.6	12.6	629	10	BE383024
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112	312.4	15.4	628	13	BI878624	BI878624 f180g04.x	185	254.8	12.6	1135	14	BQ055211
113	311.2	15.3	749	12	BG572409	BG572409 602533450	C 186	253.2	12.5	625	13	BM239250
114	309	15.2	681	14	BM723732	BM723732 K-EST0036	187	249	12.3	459	14	R33149
115	308.8	15.2	565	12	BG086244	BG086244 H3123E06-	188	248	12.2	592	12	BG160057
116	308	15.2	656	12	BE743585	BE743585 601573716	189	246.8	12.2	623	9	AL680804
117	307.8	15.2	780	10	AV757830	AV757830 AV757830	190	245.2	12.1	483	12	BF921471
118	307	15.1	326	10	BE242919	BE242919 TCAAP1E34	C 191	245	12.1	675	10	AW510247
119	306.2	15.1	754	14	BQ571766	BQ571766 UI-M-FCO-	C 192	244.4	12.1	611	10	AW149010
120	305.8	15.1	1013	10	BE618817	BE618817 601462688	C 193	243.8	12.0	688	14	BM997628
121	305	15.0	500	10	BE507076	BE507076 db90d01.Y	C 194	242.8	12.0	503	12	BF011987
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123	303.4	15.0	998	13	BM548772	BM548772 AGENCOURT	C 196	241.2	11.9	656	14	BM824921
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126	300.4	14.8	421	9	AA099707	AA099707 Z886a12.r	C 199	239.4	11.8	637	9	AL628271
127	300.2	14.8	741	9	AJ397688	AJ397688 AJ397688	200	239	11.8	568	10	AW676145
128	300	14.8	487	9	AI604044	AI604044 v18d03.Y	C 201	237.4	11.7	624	12	BF021116
129	299.4	14.8	703	14	BQ192494	BQ192494 UI-R-DR1-	C 202	237	11.7	528	14	BQ195836
130	298.4	14.7	752	10	BE540016	BE540016 601060774	C 203	236.8	11.7	617	14	BQ020122
131	298.2	14.7	630	9	AL584855	AL584855 AL584855	C 204	236	11.6	878	12	BF701483
132	295.8	14.6	612	10	BE375521	BE375521 601225407	C 205	235.6	11.6	604	10	AW027367
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135	292.8	14.4	905	12	BE893890	BE893890 601436257	C 208	233.2	11.5	905	14	BQ946104
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138	288	14.2	640	14	BQ522831	BQ522831 NISC-n118	C 211	232.6	11.5	688	10	AW871992
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140	285.8	14.1	892	14	BQ725648	BQ725648 AGENCOURT	C 213	230.6	11.4	656	12	BF232255
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142	284.8	14.0	616	9	AJ447891	AJ447891 AJ447891	C 215	227	11.2	674	9	AJ396676
143	284	14.0	679	9	AA977084	AA977084 OQ23d03.8	C 216	226.6	11.2	553	12	BG305726
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146	276.8	13.6	677	14	BQ182901	BQ182901 UI-H-EUO-	C 219	225.2	11.1	226	14	M79258
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148	274.8	13.5	689	9	AA627746	AA627746 AL627746	C 221	224.8	11.1	232	10	AW075266
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150	273.4	13.5	881	13	BI224860	BI224860 602949565	C 223	223.4	11.0	496	10	AW503320
151	273.2	13.5	685	14	BQ783261	BQ783261 UI-R-PFO-	224	223.4	11.0	682	14	BM775581
152	273	13.5	553	10	AW641341	AW641341 cm06d01.w	225	223.4	11.0			

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234	217.2	10.7	541	12	BF614186	de03a06.y	BF614186	307	177	8.7	576	14	BQ393492	BQ393492	
235	216.4	10.7	235	12	BF359280	RC6-ET008	BF359280	308	176.6	8.7	652	12	BF995881	BF995881	
236	216.4	10.7	533	9	AL595594	AL595594	AL595594	309	176.6	8.7	649	9	AA083725	AA083725	
237	215.6	10.6	571	14	BM989398	UI-H-DPO-	BM989398	310	176.6	8.7	741	12	BQ505198	BQ505198	
238	214	10.6	358	9	AA632856	np88a03.s	AA632856	311	175.8	8.7	545	9	AL633246	AL633246	
239	213	10.5	225	14	RI2762	yf58h08.r1	RI2762	312	175.6	8.7	625	9	AA083725	AA083725	
240	212.2	10.5	568	10	AW778806	ho13d06.x	AW778806	313	175.4	8.6	667	10	BB655891	BB655891	
241	211.6	10.4	710	13	BI876266	f170b11.y	BI876266	314	174.4	8.6	600	12	BQ806470	BQ806470	
242	211.2	10.4	430	10	BB712477	BB712477	BB712477	315	173.8	8.6	586	14	BQ563024	H4079D01-	
243	210.8	10.4	573	13	BI562888	fp56h11.y	BI562888	316	173.8	8.6	766	13	BI652723	BI652723	
244	210.8	10.4	744	12	EG170857	602323611	EG170857	317	173.8	8.6	898	13	BI686656	BI686656	
245	208	10.3	551	13	BM238132	K0512E07-	BM238132	318	173.8	8.6	918	14	BQ931122	BQ931122	
246	207.8	10.2	477	9	AL120795	DKF2P762E	AL120795	319	173.6	8.6	406	12	BQ901016	BQ901016	
247	207.8	10.2	718	9	AL656785	AL656785	AL656785	320	173.4	8.6	630	13	BJ061743	BJ061743	
248	207.6	10.2	504	9	AA874162	vx78f07.r	AA874162	321	172.4	8.5	556	9	AL632992	AL632992	
249	207.4	10.2	555	10	AV673706	AV673706	AV673706	322	172	8.5	574	14	BM794913	K-EST0076	
250	207	10.2	537	12	BE886298	601509983	BE886298	323	172	8.5	661	9	AL639281	AL639281	
251	206.2	10.2	539	9	AI042509	ox62f12.x	AI042509	324	171.6	8.5	890	13	BI100466	BI100466	
252	205.8	10.1	609	13	BJ048768	BJ048768	BJ048768	325	171.4	8.5	767	9	AL584137	AL584137	
253	205.4	10.1	218	14	BM745188	K-EST0019	BM745188	c	326	171.2	8.4	555	14	BQ312168	MRO-BN011
254	205.4	10.1	542	10	AW540725	C0136D09-	AW540725	327	170.6	8.4	354	14	F22929	SSC16H08	
255	205	10.1	604	9	AA218977	zr01c06.s	AA218977	328	170.6	8.4	658	14	BM778355	BM778355	
256	204.6	10.1	547	12	BQ661864	L0952D03-	BQ661864	c	329	170	8.4	621	14	BQ020192	BQ020192
257	204.6	10.1	552	9	AL672935	AL672935	AL672935	330	169.8	8.4	368	12	BQ899323	HOA18-1-D	
258	204	10.1	604	13	BI648122	603278440	BI648122	331	169.6	8.4	241	9	AA591374	AA591374	
259	203.8	10.0	539	10	AW771091	hm52a05.x	AW771091	332	169.4	8.4	896	14	BQ731602	AGENCOURT	
260	203.8	10.0	1096	17	CNS0440B	AL274412	Tetraodon	333	168.6	8.3	600	13	BI989720	BI989720	
261	203	10.0	904	12	EG666909	DRACQ04	EG666909	c	334	168.2	8.3	626	9	AI036359	AI036359
262	202.8	10.0	760	10	BI890910	ZF637-3-0	BI890910	335	167.4	8.3	375	9	AI414398	AI414398	
263	202.6	10.0	795	12	BQ740160	602630759	BQ740160	336	167.4	8.3	582	10	BE409480	601303887	
264	202.4	10.0	621	12	BF327572	MRO-BN011	BF327572	337	167.4	8.3	621	12	BQ422886	602450062	
265	202.2	10.0	489	9	AL640104	AL640104	AL640104	338	167.4	8.3	645	14	BM785807	K-EST0064	
266	201.6	9.9	288	10	BE478932	163412	BA	339	167.4	8.3	677	13	BI832000	603076072	
267	201	9.9	520	14	N79648	y281d08.r1	N79648	340	167.4	8.3	745	13	BI602130	60346251	
268	201	9.9	936	14	BQ58150	AGENCOURT	BQ58150	341	167.4	8.3	780	13	BI769127	603053718	
269	200.8	9.9	941	12	BQ163466	602338461	BQ163466	342	167.4	8.3	782	12	BQ393037	602411292	
270	200.6	9.9	334	9	AA590448	vm20d02.r	AA590448	343	167.4	8.3	811	12	BQ748163	BQ748163	
271	199.6	9.8	666	12	BF158385	f132b05.y	BF158385	344	167.4	8.3	848	12	BQ393838	602416694	
272	199.4	9.8	350	9	AA617999	np88b03.s	AA617999	345	167.4	8.3	864	14	BQ432214	BQ432214	
273	198.8	9.8	936	14	BQ642076	AGENCOURT	BQ642076	346	167.4	8.3	868	12	BE782263	BE782263	
274	198	9.8	559	14	BM746954	K-EST0021	BM746954	347	167.4	8.3	889	14	BQ214346	BQ214346	
275	197.4	9.7	549	10	AW196832	xb13e08.x	AW196832	348	167.4	8.3	892	14	BQ883431	BQ883431	
276	196.6	9.7	1020	14	BQ22272	AGENCOURT	BQ22272	349	167.4	8.3	898	13	BI909933	BI909933	
277	195.8	9.7	300	17	A2313089	1M0029118	A2313089	350	167.4	8.3	919	12	BQ768734	602743179	
278	195.8	9.7	550	13	BJ033483	BJ033483	BJ033483								
279	195	9.6	555	14	BM743244	K-EST0016	BM743244								
280	194.6	9.6	686	10	AW071056	xa32f07.x	AW071056								
281	193	9.5	371	9	AA546195	vk05b09.r	AA546195								
282	192	9.5	371	9	AW767124	da63c02.y	AW767124								
283	190	9.4	583	10	BQ247905	602359822	BQ247905								
284	188.2	9.3	514	17	AQ169618	HS_3181.B	AQ169618								
285	187.8	9.3	610	10	BE299569	600944483	BE299569								
286	187	9.2	203	14	BM835929	K-EST0111	BM835929								
287	187	9.2	711	12	BG871080	602790249	BG871080								
288	186.4	9.2	500	13	BI987135	3192-10.M	BI987135								
289	186.2	9.2	442	10	AW377517	QV0-CT022	AW377517								
290	185.6	9.2	1192	12	BG112462	602282053	BG112462								
291	185.2	9.1	518	9	AA825580	od57f01.s	AA825580								
292	184.2	9.1	595	10	AW175372	f135c09.y	AW175372								
293	184.2	9.1	649	13	BJ042518	BJ042518	BJ042518								
294	183.6	9.1	640	10	BB624364	BB624364	BB624364								
295	182.4	9.0	184	9	AA911425	o871b06.s	AA911425								
296	182.2	9.0	904	12	BF099638	601751661	BF099638								
297	181.6	9.0	853	12	BF672611	602152196	BF672611								
298	181.4	8.9	537	13	BJ065403	BJ065403	BJ065403								

RESULT 1

EQ677542

LOCUS

DEFINITION

AGENCOURT_8212225 NIH_MGC_112 Homo sapiens CDNA clone IMAGE:6260712

5', mRNA sequence.

ACCESSION

BQ677542

VERSION

BQ677542.1

GI-21970221

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 903)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

903 bp

mRNA

linear

EST 15-JUL-2002

ALIGNMENTS

RESULT 1	903 bp	linear	EST 15-JUL-2002
LOCUS	AGENCOURT_8212225	NIH_MGC_112	Homo sapiens
DEFINITION	5', mRNA sequence.		
ACCESSION	BQ677542		
VERSION	BQ677542.1	GI:21790221	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 903)		
JOURNAL	NIH-MGC http://mgi.nci.nih.gov/		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgaabs@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2420 row: e column: 01
 High quality sequence stop: 660.
 Location/Qualifiers

FEATURES

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 /db_xref="taxon:9606"
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 /clone_lib="NIH_MGC_112"
 /tissue_type="melanotic melanoma, cell line"
 /lab_hosts="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dr priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH MGC Library."

BASE COUNT 232 a 229 c 242 g 198 t 2 others
 ORIGIN

Query Match 38.0%; Score 770; DB 14; Length 903;
 Best Local Similarity 97.0%; Pred. No. 8.9e-155;
 Matches 848; Conservative 0; Mismatches 17; Indels 9; Gaps 6;

Qy 470 AGACCCGCTGGTGGTCCCGCCGACGAGAAACGGCGCTTTGGGCGAGCGGAGGGGCTG 529

Db 1 AGACCCGCTGGTGGTCCCGCCGACGAGAAACGGCGCTTTGGGCGAGCGGAGGGGCTG 60

Qy 530 GCAGCGATAGCACTCTCTGGAAACGTCACAGCTAACTTCTGCCCGCCGAGCTCGAATCCC 589

Db 61 GCAGCGATAGCACTCTCTGGAAACGTCACAGCTAACTTCTGCCCGCCGAGCTCGAATCCC 120

Qy 590 ACCCGCTCTTGAAGGCTGCTCAGCTCAACAGCTCAACCCGAAAGAGTTTGAGTGGG 649

Db 121 ACCCGCTCTTGAAGGCTGCTCAGCTCAACAGCTCAACCCGAAAGAGTTTGAGTGGG 180

Qy 650 ATCTGAAAGCGGGGCTGTTTCATCATCAAGAGTACTCTGAGAGCGACATCCACCGCT 709

Db 181 ATCTGAAAGCGGGGCTGTTTCATCATCAAGAGTACTCTGAGAGCGACATCCACCGCT 240

Qy 710 CCATTAAAGTACTCCATCTGGGTAGCAGAGCAGCGCAACAGCGCTGACAGCGCT 769

Db 241 CCATTAAAGTACTCCATCTGGGTAGCAGAGCAGCGCAACAGCGCTGACAGCGCT 300

Qy 770 TCCGCTGATGAGCAGGAGGGGCGCTTACCTGCTCTTCAGGCTCAATGGGAGTGGGC 829

Db 301 TCCGCTGATGAGCAGGAGGGGCGCTTACCTGCTCTTCAGGCTCAATGGGAGTGGGC 360

Qy 830 ATTTTGTGGGGTGGCGAGATGAAGTCCCGTGGACTACGGCAACAGTCCCGGGTCT 889

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Qy 890 GGTCTCAGGACAAT-GGAAGGGAGTTTGTATGTCCTCAGTGGATTTTGTAAAGGATGA 948

Db 421 GGTCTCAGGACAATGGAAGGGAGTTTGTATGTCCTCAGTGGATTTTGTAAAGGATGA 480

Qy 949 CCCAATAACCAAGCTCCGGCACAATCAGGCTGAGATACGCAACAACCCGCTCACAAAC 1008

Db 481 CCCAATAACCAAGCTCCGGCACAATCAGGCTGAGATACGCAACAACCCGCTCACAAAC 540

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RESULT 2

BQ682082

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ682082
 AGENCOURT_8185508 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6263040
 5', mRNA sequence.

BO682082
 BO682082.1 GI:21794761
 EST.

human.
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 889)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs@mail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2426 row: f column: 01

High quality sequence stop: 567.

FEATURES

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 /db_xref="taxon:9606"
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 /clone_lib="NIH_MGC_112"
 /tissue_type="melanotic melanoma, cell line"
 /lab_hosts="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dr priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH MGC Library."

BASE COUNT 223 a 238 c 248 g 178 t 2 others
 ORIGIN

Query Match 35.8%; Score 725.8; DB 14; Length 889;

Best Local Similarity 97.0%; Pred. No. 2.7e-145;

Matches 781; Conservative 0; Mismatches 19; Indels 5; Gaps 4;

Qy 470 AGACCCGCTGGTGGTCCCGCCGACGCAACAGAAACGCGGCTTTGGGCGAGCGGAGGGCTG 529

Db 1 AGACCCCGCTGGTGGTCCCGACGACAGAAACCGCGCTTTGGGCAGAGCGGAGCGCTG 60
QY 530 GCAGCGATAGCAACTCTCTCTGGAACCTCAGAGCTTAATCTGCCCCCAGCGGTGCAATCCC 589
Db 61 GCAGCGATAGCAACTCTCTCTGGAACCTCAGAGCTTAATCTGCCCCCAGCGGTGCAATCCC 120
QY 590 ACCCGCTCTTGAAGAACTGAAGCTGCTCACAGCTACAAACCCGAAAGATTTGAGTGA 649
Db 121 ACCCGCTCTTGAAGAACTGAAGCTGCTCACAGCTACAAACCCGAAAGATTTGAGTGA 180
QY 650 ATCTGAAGCGGGCGTGTCTTCATCATCAAGAGCTACTCTGAGGACGACATCCACGCT 709
Db 181 ATCTGAAGCGGGCGTGTCTTCATCATCAAGAGCTACTCTGAGGACGACATCCACGCT 240
QY 710 CCATTAAGTACTTCATCTGCTGTAGCAGACGAGCAGCGCAACAGCGCTTGACAGCGCT 769
Db 241 CCATTAAGTACTTCATCTGCTGTAGCAGACGAGCAGCGCAACAGCGCTTGACAGCGCT 300
QY 770 TCCGCTGCATGAGCAGAGCGGCGCTCTACCTGCTCTTCAAGCTCAATGGAGTGGC 829
Db 301 TCCGCTGCATGAGCAGAGCGGCGCTCTACCTGCTCTTCAAGCTCAATGGAGTGGC 360
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Db 361 ATTTTGTGGGTGGCGGAGATGAATGCCCGTGGACTAGGACACGACGCGGGTCT 420
QY 890 GGTCTCAGGACAACTGCAAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGATGTAC 949
Db 421 GGTCTCAGGACAACTGCAAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGATGTAC 480
QY 950 CCAATAACAGCTCCGCGACATCAGGCTGGAGATAACGACAAACAAACCGGTACAAACT 1009
Db 481 CCAATAACAGCTCCGCGACATCAGGCTGGAGATAACGACAAACAAACCGGTACAAACT 540
QY 1010 CCGGGACACCCAGGAGGTGCCCTTAGAAAAAGCAAGCAAGTCTGAAATATCAGTT 1069
Db 541 CCGGGACACCCAGGAGGTGCCCTTAG - AAAAGCAAGCAAGTCTGAAAA - TATCAGTT 598
QY 1070 CCTACAGCACACAACTCCATCTTCAGCAGCTTTGCTCACTACGAGAGCGCA - GAG 1127
Db 599 CCTACAGCACACAACTCCATCTTCAGCAGCTTTGCTCACTACGAGAGCGCAAGG 658
QY 1128 GAGGAGAGGTGGTGGCAGAGAACGGCAGAGTGAACAAACAAATGAGGCGCAACAGT 1187
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QY 1188 TTCTTACATGTTCTAAAGTTTGAATTTGAAACAGATTTTAAACACGTTGCTTGGTCAGC 1247
Db 718 TTCTTACATGTTCTAAAGTTTGAATTTGAAACAGATTTTAAACACGTTGCTTGGTCAGC 777
QY 1248 TCCAGTGTGCTCCCGTGGGGG 1272
Db 778 TCCCGTGGGGGNTCCCCCGGGGG 802

RESULT 3
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LOCUS
DEFINITION BO421505 928 bp mRNA linear EST 23-MAY-2002
5', mRNA sequence.
ACCESSION BO421505
VERSION BO421505.1 GI:21116820
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 928)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13234 row: g column: 22
High quality sequence stop: 578.

FEATURES
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/tissue_type="large_cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 Kb. Library constructed by Life
Technologies."

BASE COUNT 243 a 230 c 233 g 221 t 1 others
ORIGIN
Query Match 34.6%; Score 701.4; DB 14; Length 928;
Best Local Similarity 98.0%; Pred. No. 4.6e-140;
Matches 732; Conservative 0; Mismatches 11; Indels 4; Gaps 2;

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Db 12 CCCACGGTGCATCCACCCCGTCTTTGAAAACTGAAGGCTGCTCACAGCTACAAACC 71
QY 633 GAAAGAGTTTGAGTGAATCTGAAAAGCGGGCTGTGTTTCATCATCAAGAGTACTCTGA 692
Db 72 GAAAGAGTTTGAGTGAATCTGAAAAGCGGGCTGTGTTTCATCATCAAGAGTACTCTGA 131
QY 693 GGACGACATCCACCGCTCCATTAAGTACTCCATCTGTTGTAGCAGAGCACGGCAACAA 752
Db 132 GGACGACATCCACCGCTCCATTAAGTACTCCATCTGTTGTAGCAGAGCACGGCAACAA 191
QY 753 GCGCTTGACAGCGCTTCCGCTGCATGAGCAGAGGGGCGCTTACCTGCTCTTCAG 812
Db 192 GCGCTTGACAGCGCTTCCGCTGCATGAGCAGAGGGGCGCTTACCTGCTCTTCAG 251
QY 813 CGTCAATGGAGTGGGCATTTTGTGGGTGGCGGAGATGAAGTCCCGCTGAGTACGG 872
Db 252 CGTCAATGGAGTGGGCATTTTGTGGGTGGCGGAGATGAAGTCCCGCTGAGTACGG 311
QY 873 CACAGTGGCGGGTCTGGTCTCAGGACAAAGTGGAAAGGGGAAGTTTGAATGCCAGTGGAT 932
Db 312 CACAGTGGCGGGTCTGGTCTCAGGACAAAGTGGAAAGGGGAAGTTTGAATGCCAGTGGAT 371
QY 933 TTTTGTTAAGATGTACCCAAATTAACAGCTCCGCGACATCAGGCTGGAGATAACGACAA 992
Db 372 TTTTGTTAAGATGTACCCAAATTAACAGCTCCGCGACATCAGGCTGGAGATAACGACAA 431
QY 993 CAACCGGTGACAAACTCCCGGACACCCAGGAGTGCCTTTAGAAAAAGCCCAAGCAAGT 1052
Db 432 CAACCGGTGACAAACTCCCGGACACCCAGGAGTGCCTTTAGAAAAAGCCCAAGCAAGT 491
QY 1053 GCTGAAAAATATCAGTTCTTACAGCACAACCTCCATCTTCGACGACTTTGCTCACTA 1112
Db 492 GCTGAAAAATATCAGTTCTTACAGCACAACCTCCATCTTCGACGACTTTGCTCACTA 551
QY 1113 CGAGAGCGGCA - GAGAGAGAGGAGTGGTGGCAGAGAAACGGCAGAGTGCAGAAACAA 1171
Db 552 CGAGAGCGGCA - GAGAGAGAGGAGTGGTGGCAGAGAAACGGCAGAGTGCAGAAACAA 611
QY 1172 ATGAGGCGGAACAGATTTCTTACATGTTCTTAACGTTTGTGCTTTGAAACAGTTTAAACA 1231
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Qy 1232 CGTGTCTGTGTCAGCTCCAGTGTGTCTCCCGTCCGGGGGTGAGTGTTCGATCTTTGC 1291
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RESULT 4
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LOCUS 601434159F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918154 5',
DEFINITION mRNA sequence.
ACCESSION BE894361
VERSION BE894361.1 GI:10356650
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1109)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9745 row: n column: 11
High quality sequence stop: 725.
Location/Qualifiers
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/clone="IMAGE:3918154"
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/tissue_types="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 291 a 303 c 273 g 242 t
ORIGIN
Query Match 33.3%; Score 674.6; DB 12; Length 1109;
Best Local Similarity 92.9%; Pred. No. 2.5e-134;
Matches 763; Conservative 0; Mismatches 49; Indels 9; Gaps 5;

Qy 552 AAACGTCAGCCTAATTCTGCCCGCCAGCGTCGAATCCACCCCGCTCTGTAAGAACTGAA 611
Db 1 AAACGTCAGCCTAATTCTGCCCGCCAGCGTCGAATCCACCCCGCTCTGTAAGAACTGAA 60

Qy 612 GCCTGCTCAGAGCTACACCCGAAAGAGTTTGTAGTGGATCTGAAAGCGGCGTGTGT 671
Db 61 GCCTGCTCAGAGCTACACCCGAAAGAGTTTGTAGTGGATCTGAAAGCGGCGTGTGT 120

Qy 672 CATCATCAAGAGTACTCTGAGGACGACATCCACCGC--TCCATTAAAGTACTCCATCTGGT 730
Db 121 CATCATCAAGAGTACTCTGAGGACGACATCCACCGGCTCCATTAGTACTCCATCTGGT 180

Qy 731 GTAGCAGAGCAGCGCAACAGCGCTTGGACAGCGCTTCCGTCGATGACGACGAAG 790
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Qy 791 GGCCGCTACCTCTCTTACGCTCAATGGAGTGGGCATTTTGGGGTGGCCGAGA 850

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Db 241 GGCCCGTCTACCTGCTCTTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCCGAGA 300
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Qy 971 TCAGGCTGGAGATTAAGCAACAACCGGTCAAACTCCCGGACACCCAGAGGTGC 1030
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Db 481 CCTTAGAAAAGCCAAAGTGTCTGAAAATTTATCAGTCTCTCAAGCAACACACCTCCA 540
Qy 1091 TCTTCGACGACTTTGCTCACTAGAGAAAGCCCA--GAGGAGGAGGAGGTGTGGCAAGG 1149
Db 541 TCTTCGACGACTTTGCTCACTAGAGAAAGCCCA--GAGGAGGAGGAGGAGGTGTGGCAAGG 600
Qy 1150 AACGGCAGAGTCCGAACAAA--CAATGAGGCGCAACCAAGTTCTTACATGTCTTAACGTTT 1208
Db 601 AACGGCAGAGTCCGAACAAA--CAATGAGGCGCAACCAAGTTCTTACATGTCTTAACGTTT 660
Qy 1209 GACTTTGA--AAACAGTTTAAACACAGTGTCTTGGTCAGTCTCCAGTGTGTGTCGCCGTG 1266
Db 661 GACTTTGAACACAGTTTAAACACAGTGTCTTGGTCAGTCTCCAGTGTGTGTCGCCGTG 720
Qy 1267 CGGGGGTTGAGTGTGTCATCTTTGCCCTTTCTTGTGCTTG---ATTTTGGCCCAAGTGA 1322
Db 721 CGGGGGTTGAGTGTGTCATCTTTGCCCTTTCTTGTGCTTG---ATTTTGGCCCAAGTGA 780
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Db 781 TCTGCCTTCATTGGACGTTCTCCACGGCATAATAACCCGT 821

RESULT 5
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LOCUS 601434159F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919118 5',
DEFINITION mRNA sequence.
ACCESSION BE892982
VERSION BE892982.1 GI:10353885
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 852)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9748 row: f column: 15
High quality sequence stop: 643.
Location/Qualifiers
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/db_xref="taxon:9606"
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/tissue_type="melanotic melanoma"

FEATURES
source

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/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT      223 a   199 c   167 g   263 t
ORIGIN

Query Match      32.1%; Score 650.8; DB 12; Length 852;
Best Local Similarity 94.9%; Pred. No. 3.2e-129;
Matches 748; Conservative 0; Mismatches 32; Indels 8; Gaps 7;

Qy 969 CATCAGCTCGAGATTAACGACAAACAAACCGGTGTCACAACTCCCGGACACCCAGGAGGT 1028
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Qy 1029 GCCCTTAGAAAAAGCCAAAGCGTGTGAAATATCATGTTCTCTACAGGACACAACTC 1088
Db 61 GCCCTTAGAAAAAGCCAAAGCGTGTGAAATATCATGTTCTCTACAGGACACAACTC 120

Qy 1089 CATCTTCGACGACTTTGCTCACTACGAGAGCGCA - GAGGAGGAGGAGGTGGTGCACAA 1147
Db 121 CATCTTCGACGACTTTGCTCACTACGAGAGCGCGCAGGAGGAGGTGGTGCACAA 180

Qy 1148 GGAACGGCAGAGTCGAAACAAACAAATGAGGGCGAACGAGTTCTTACATGTTCTAACGTT 1207
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Qy 1208 TGACTTTGAAACAGGTTTAAACACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1267
Db 241 TGACTTTGAAACAGGTTTAAACACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300

Qy 1268 GGGGGTTGAGTGTTCATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1327
Db 301 GGGGGTTGAGTGTTCATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

Qy 1328 ATTTATTTGTAATTTTCTATGTAATTAATTAATCTGTTAGAGTCTACTAATAAGGAGTATT 1387
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Qy 1388 TTTTGTGTCAGCTTATCAATCAGACTGATCTATGTAATGTAATGTAATGTAATGTAATGTAATG 1447
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Qy 1448 AAAGCATCTATTTTGGCAGAAATTTGTTTCTTAAATTCAGTCACTTTGATAT - TCTGTGAG 1506
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Qy 1507 ACTTCATATTTCTCATCCCTTTATTTGCTTTTATAGCAACATAGAAACCATGAGTCAATTT 1566
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Qy 1567 TGTCAATTAGAGTATTCGATAAATCTCTTGAAATCTGAAATCTGAAATCTGAAATCTGAAATCT 1626
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Qy 1627 TTTTGTTCATCTGATTTGTCATTTTATTTATCTGTTATCTGTTATCTGTTATCTGTTATCTG 1685
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Qy 1686 - CCCATTTGATTTTCTGCTAGACAGATAAATCTTTTAAATTTTCAAATTTGGCAGACACTT 1744
Db 718 CCCATTTGACTTCTCTGCTAGACCGCTTACCCCTT - ATTTTCCACATTTCCGCCGACCTTT 776

Qy 1745 TTTTGTCTT 1752
Db 777 TCTTCTCT 784

RESULT 6
AV079675 1014 bp mRNA linear EST 24-OCT-2001
LOCUS AV079675 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
DEFINITION
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clone 2210410K23, mRNA sequence.

AV079675 GI:16381140

AV079675.2

EST.

house mouse.

Mus musculus

Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1014)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.

, Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda

, M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Onno,M.,

Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki

, Tagami,M., Tagawa,A., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,

Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

Unpublished (2001)

On Jun 25, 1999 this sequence version replaced gi:5211123.

Contact: Yoshihide Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/

, M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura

, S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and

Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

, Y. and Hayashizaki,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara

Computer-based methods for the mouse full-length cDNA

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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa

, K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and

Hayashizaki,Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp/) for

further details.

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Location/Qualifiers

1. .1014

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/clone="2210410K23"

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/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia

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RI; 1st strand cDNA was primed with a Not I - oligo(dT)

primer [5'

TGTTACCAATCTGAAGTGGAGCGCGGCAATGTTTTTTTTTTTTTTTTTTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Patima Bonaldo."

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BASE COUNT      266 a      238 c      252 g      256 t      2 others
ORIGIN

Query Match      32.0%; Score 648.8; DB 9; Length 1014;
Best Local Similarity 82.2%; Pred. No. 8.6e-129;
Matches 822; Conservative 0; Mismatches 159; Indels 19; Gaps 6;

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Qy 586 TCCACCCCGCTCTTGAATAAATGAAGCTGTACAGCTACAAACCCGAAAGAGTTTGAG 645
Db 197 TCCACCCGTCTCTGGAAACCTGAAAGCTGCCACAGCTATAACCTTAAAGAGTTTCAG 256
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Qy 826 GGGCAATTTCTGGGCTGGCGAGATGAAGTCCCGTGGAGTACGACAGCAGCGCGG 885
Db 437 GGACATTTCTGGGCTGGCGAGATGAAGTCCCGTGGAGTATGGCACCAGCGCTGG 496
Qy 886 GTCTGGTCTCAGGCAAGTGGAAAGGGAAGTTGATGTCCAGTGGATTTTGTGTAAGGAT 945
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Qy 946 GTACCCAAATACCGACTCCGGCAGATCAGGCTGGAGATATACGACAAACCCGTCACA 1005
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RESULT 7
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DEFINITION AL574115 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI040YK06 3
prime, mRNA sequence.
ACCESSION AL574115
VERSION    AL574115
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 661)
AUTHORS   Li, W.-B., Gruber, C., Jesse, J., and Polaves, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 Evry cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                    vector. Library was normalized. Library was constructed by
                    Life Technologies. Contact : Feng Liang Life Technologies,
                    a division of Invitrogen 9800 Medical Center Drive
                    Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                    Email : fliang@lifetech.com URL :
                    http://fulllength.invitrogen.com"
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BASE COUNT      119 a      179 c      178 g      181 t      4 others
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Query Match      31.8%; Score 644.6; DB 9; Length 661;
Best Local Similarity 99.1%; Pred. No. 7.1e-128;
Matches 665; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
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Qy 527 CTGCGCGGATAGCACTCTCTGGAAACCTCCAGACCTTAATCTGCCCCCAGCGTCCAAT 586
Db 661 CTGCGCGGATAGCAATCTCTGGAAACCTCCAGACCTTAATCTGCCCCCAGCGTCCAAT 602
Qy 587 CCCACCCCGCTCTTTGAAATAACTGAAAGCTCTCACAGCTACAAACCCGAAAGAGTTTCA 646
Db 601 CCCACCCCGCTCTTTGAAATAACTGAAAGCTCTCACAGCTACAAACCCGAAAGAGTTTCA 542
Qy 647 GGAATCTGAAAAGCGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGAGCAGATCCACC 706
Db 541 GGAATCTGAAAAGCGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGAGCAGATCCACC 482
Qy 707 GCTCCATTAGTACTCCATCTGTTGTAGCAGACGACGCAACGCGCTCGACAGCG 766
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Db 1 G 1

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DEFINITION
AL515908 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA001YB18 3
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ACCESSION
AL515908.1 GI:12779401
VERSION
EST.
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1068)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 9106 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library is not normalized, but is the control for
the normalized libraries. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
filiang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 382 a 217 c 187 g 275 t 7 others
ORIGIN
Query Match 31.2% Score 633.4; DB 9; Length 1068;
Best Local Similarity 98.0%; Pred. No. 1.7e-125;
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Matches 646; Conservative 5; Mismatches 6; Indels 2; Gaps 1;
Qy 1370 CACTAATAAAGAGATTTTGTGTCAGCTTATCAATCAGACTGATCTAATGTGAAT 1429
Db 1068 CACTAATAAAGRGTA--TTTGTGTCAGCTTATCAATCAGACTGATCTAATGTGAAT 1011
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Qy 1490 ATTTCATATTTCTGTGAGACTTCATATTTCTCATCCCTTTATTTGCTTTTAGCAACATAA 1549
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Qy 1850 GATGTGTGGAGGAACCTGGAAGGCTTTTAGGCTCTGCTCAGGCTCGGCAATCTTTGTTG 1909
Db 590 GATGTGTGGAGGAACCTGGAAGGCTTTTAGGCTCTGCTCAGGCTCGGCAATCTTTGTTG 531
Qy 1910 TTTGCACATCTTTTAAATTTTACACCTTTTCTTAAGAAATCTTAATGCCGTCTTAAGTTT 1969
Db 530 TTTGCACATCTTTTAAATTTTACACCTTTTCTTAAGAAATCTTAATGCCGTCTTAAGTTT 471
Qy 1970 TTATACCAATATGCTGAGCTTTAAGTGTAGGATCTGGTAGTACAGACAGTGTGATGA 2028
Db 470 TTATACCAATATGCTGAGCTTTAAGTGTAGGATCTGGTAGTACAGACAGTGTGATGA 412

RESULT 9
AW001012/c
LOCUS
DEFINITION
AW001012 wr91e06.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2495074 3,
similar to TR:064526 YUP8H12R.13 PROTEIN. ;, mRNA sequence.
ACCESSION
AW001012
VERSION
AW001012.1 GI:5847928
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 684)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/JLNL at:
```

www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 1194 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 476.

FEATURES

Source
1. .684
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2495074"
/clone_lib="NCI CGAP_Kid11"
/lab_host="DH10B"
/notes="Organ: kidney; Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 175 a 178 c 160 g 171 t

ORIGIN

Query Match 31.0%; Score 628.8; DB 10; Length 684;
Best Local Similarity 97.8%; Pred. No. 1.7e-124;
Matches 669; Conservative 0; Mismatches 12; Indels 3; Gaps 3;
QY 725 TCTGGTGTAGCAGACGCGCAACAGCGCTGGACAGCGCTTCGGCTGCATGAGCA 784
DB 683 TCTGGTGTAGCAGACGCTGCACAAACAGCGCTGCACAGCGCTTCGGCTGCATGAGCA 624
QY 785 GCAAGGGCCGCTTACCTGCTCTTACGCGTCAATGGAGTGGGCAATTTTGTGGGGTGG 844
DB 623 GCAAGGGCCGCTTACCTGCTCTTACGCGTCAATGGAGTGGGCAATTTTGTGGGGTGG 564
QY 845 CCGAGATGAAGTCCCGCTGGACTACGCGACAGTGGCGGGGTCTGGTCTCAGGACAACT 904
DB 563 CCGACATCAAGTCCCGCTGGACTATGCGCACAGTGGCGGGGTCTGGTCTCAGGACAACT 504
QY 905 GGAAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGGATGTACCCATTAACCACTCC 964
DB 503 GGAAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGGATGTACCCATTAACCACTCC 444
QY 965 GGCACATCAGGCTGAGAAATACGACAAACACCGTGCACAACTCCCGGACACCCAGG 1024
DB 443 GGCACATCAGGCTGAGAAATACGACAAACACCGTGCACAACTCCCGGACACCCAGG 384
QY 1025 AGGTGCCCTTAGAAAAAGCCCAAGCAAGTGTGAAATTTATCAGTTCTTACAGCACACAA 1084
DB 383 AGGTGCCCTTAGAAAAAGCCCAAGCAAGTGTGAAATTTATCAGTTCTTACAGCACACAA 324
QY 1085 CTTGATC- TTGCGAGCTTTGCTCATTACAGAGAGCGCCA- GAGGAGGAGGAGTGGTG 1142
DB 323 CTTGATCATTGAGCACTTTGCTCATTACAGAGAGCGCCAGGAGGAGGAGTGGTG 264
QY 1143 CGCAGGAACCGCAGTGCAGAAACAAATGAGGGGCAACAGTCTTACATGTTCTTA 1202
DB 263 CGCAGGAACCGCAGTGCAGAAACAAATGAGGGGCAACAGTCTTACATGTTCTTA 204
QY 1203 ACGTTTGTGATTTGAAACAGTTTAAACACAGTGTGCTTGGTGCAGTCCAGTGTGCTGCC 1262
DB 203 ACGTTTGTGATTTGAAACAGTTTAAACACAGTGTGCTTGGTGCAGTCCAGTGTGCTGCC 144
QY 1263 CGTGGGGGGTGTGATGTGATCTTTGCGCTTCTTGTGCTTGAATTTTGGCCGAGTGA 1322
DB 143 CGTGGGGGGTGTGATGTGATCTTTGCGCTTCTTGTGCTTGAATTTTGGCCGAGTGA 84
QY 1323 TCTGATTTATTTGATCTTTTCTATGATTTATTAATCTGTGAGAGTCACTAATAAAGGA 1382
DB 83 TCTGATTTATTTGATCTTTTCTATGATTTATTAATCTGTGAGAGTCACTAATAAAGGA 24
QY 1383 GTATTTTTTTTGTGAGCTTATCA 1406

Db 23 GTA-TTTTTTTTGTGAGCTTATCA 1

RESULT 10

AV726565
LOCUS
DEFINITION AV726565 HTC Homo sapiens cDNA clone HTCAE08 5', mRNA sequence.
ACCESSION AV726565
VERSION AV726565.1 GI:10835986
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 932)
AUTHORS Gu, Y., Feng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.
TITLE Homo sapiens cDNA HTC clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@hgsc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

Source
1. .932
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTCAE08"
/clone_lib="HTC"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 240 a 166 c 179 g 340 t

ORIGIN

Query Match 30.9%; Score 626.6; DB 10; Length 932;
Best Local Similarity 97.0%; Pred. No. 5e-124;
Matches 679; Conservative 0; Mismatches 17; Indels 4; Gaps 4;
QY 1329 TTTATTTGTACTTTTTTCTATGATTAATCCTGTAGAAGTCACCTAATAAGGAGTATTT 1388
DB 2 TTTACTCGTACTTTTCTATGATTAATCCTGTAGAAGTCACCTAATAAGGAGTA-TT 60
QY 1389 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAATGTAAAGTATCTTTAAAAACA 1448
DB 61 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAATGTAAAGTATCTTTAAAAACA 120
QY 1449 AAGCATCTATTTGGCAGAAATGTGTTCTTAATTCAGTCATTTGATATTCGTGAGAC 1508
DB 121 AAGCATCTATTTGGCAGAAATGTGTTCTTAATTCAGTCATTTGATATTCGTGAGAC 180
QY 1509 TTCAATTTCTCATCCCTTTTATTTGCTTTTAGCAAAACATAAGAAACCATCAGTCATTTT 1568
DB 181 TTCAATTTCTCATCCCTTTTATTTGCTTTTAGCAAAACATAAGAAACCATCAGTCATTTT 240
QY 1569 TCATTAGAGTATTCGATAAAATCTCTGAAAATCTGAAATCTGAATCAAAAGGTAAATGATTT 1628
DB 241 TCATTAGAGTATTCGATAAAATCTCTGAAAATCTGAAATCTGAATCAAAAGGTAAATGATTT 300
QY 1629 TTTCTTCATTTCTGATTTGTCTATTTATTTATCTGTTATCTGGTCTTAAAGTCTAAATTTACCC 1688
DB 301 TTTCTTCATTTCTGATTTGTCTATTTATTTATCTGTTATCTGGTCTTAAAGTCTAAATTTACCC 360
QY 1689 ATTTGATTTTCTGCTAGACAGATAACTTTTAATTTTCAAAATTTTGCAGACACTTTTTT 1748

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Db 361 ATTGTATTTTCTGTAGACAGATAACTCTTAATTTTCAAAATTTTGGCAGACACTTTNTT 420
QY 1749 TTTTATTTTGAATACTTTCTTCCAGATCTGTGTCCTCACTGAACGCCACCGCTCCCTC 1808
Db 421 TTTTATTTTGAATACTTTCTTCCAGATCTGTGTCCTCACTGAACGCCACCGCTCCCTC 480
QY 1809 ACTGTCCTGGTCCGATTTGGGCTGATGGTGTGGGCAATGATGTGGAGGAATGGA 1868
Db 481 ACTGTCCTGGTCCGATTTGGGCTGATGGTGTGGGCAATGATGTGGAGGAATGGA 540
QY 1869 AGGTGCTTTAGTCTGGTTCAGGCTCGGCATCTTTGTTGTCACATCTTTTAAAT 1928
Db 541 AGGTGCTTTAGTCTGGTTCAGGCTCGGCATCTTTGTTGTCACATCTTTTAAAT 598
QY 1929 TTTTACACCTTTTCTTAAGAAATTTCTAATGCCGTCTTAAGTTTATACCAATATGCTGAG 1988
Db 599 TTTTACACCTTTTCTTAAGAAATTTCTAATGCCGTCTTAAGTTTATACCAATATGCTGAG 657
QY 1989 CTTTAAAGTGTAGATCTGGTGTAGTACAGACAGTGTGATGGA 2028
Db 658 CTTTAAAGTGTAGATCTGGTGTAGTACAGACAGTGTGATGGA 697

RESULT 11
BM423045
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
rhesus monkey.
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheciae; Macaca.
REFERENCE
Katze, M.G., Bumgarner, R., Korth, M., Feldman, R., Amjadi, M. and
Holzman, T.
TITLE
Expressed sequence tags from Rhesus macaque spleen
JOURNAL
Unpublished (2002)
COMMENT
Contact: Holzman T
Katze Lab
University of Washington
Box 358070, Seattle, WA 98195-8070, USA
Tel: 206 732 6156
Fax: 206 732 6055
Email: ted@locke.hs.washington.edu
PLAYEL_D11 1479 bases; 23.2 mean phred score.

FEATURES
source
1..1479
/organism="Macaca mulatta"
/db_xref="taxon:9544"
/clone_lib="Rhesus"
/tissue_type="spleen"
/dev_stage="adult"
/notes="Vector: pBluescript SK; SIV-associated
centroblastic non-Hodgkin's lymphoma"

BASE COUNT 561 a 342 c 359 g 217 t
ORIGIN

Query Match 30.8%; Score 623.8; DB 13; Length 1479;
Best Local Similarity 93.9%; Pred. No. 1.9e-123;
Matches 660; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

QY 467 CCAGACCCCTGGTGGTCCCGCCAGCAACAGAACCGCGGTGTGGCAGCGAGGGG 526
Db 31 CCCAGAACCCCTGGTGGTCCCGCCAGCAACAGAACCGCGGTGTGGCAGCGAGGGG 90
QY 527 CTGGCAGCGATAGCACTCTCTGGGAACCTCCAGCCTAATTTGCCCCCAGCGTGAAT 586
Db 91 CTGGCAGGTAGCACTCTCTGGGAATGTCCAGCCTAATTTCCACCCCGCGTGAAT 150
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QY 587 CCCACCCCGTCTCTGAAAAAATGAAAGGCTGTCTCAGCTACAAACC-GAAAGAGTTTGAG 645
Db 151 CCCACCCCTGTCTCTGAAAAAATGAAAGGCTGTCTCAGCTATAAACCCTTAAAGAGTTTGAC 210
QY 646 TGGAAATCTGAAAAAGCGGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGACATCCAC 705
Db 211 TGGAAATCTGAAAAAGCGGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGATGACATCCAT 270
QY 706 CGCTCCATTAAGTACTTCCATCTGGTGTAGCACAGACGCGCAACAAGCGCTTGGACAGC 765
Db 271 CGCTCCATTAAGTACTTCCATCTGGTGTAGCACAGACGCGCAACAAGCGCTTGGACAGC 330
QY 766 GCGTTCCTGTCATGAGCAGCAAGGGGCCGCTTACCTGCTCTTTCAGCGTCAATGGAGT 825
Db 331 GCGTTCCTGTCATGAGCAGCAAGGGGCCGCTTACCTGCTCTTTCAGCGTCAATGGAGT 390
QY 826 GGGCATTTTTTGTGGGTGGCGCAGATGAAGTCCCGCTGGAGTACGGCACCAAGTGGCGGG 885
Db 391 GGGCATTTTTTGTGGGTGGCGCAGATGAAGTCCCGCTGGAGTACGGCACCAAGTGGCGGG 450
QY 886 GTCTGCTCTCAGGACAAAGTGGAAAGGGGAAATTTGATGTCCAGTGGATTTTGTAAAGGAT 945
Db 451 GTCTGCTCTCAGGACAAAGTGGAAAGGGGAAATTTGATGTCCAGTGGATTTTGTAAAGGAT 510
QY 946 GTACCCAATAACAGCTCCGGCACATCAGGCTGGAGATAACGACAAACAACCGGTCA 1005
Db 511 GTGCCCCAATAACAGCTCCGGCACATCAGCTGGAGATAACGACAAACAACCGGTCA 570
QY 1006 AACTCCCGGACACCCAGGAGTGGCCCTTAGAAAAAGCAAGCAAGTGTGAAAAATTATC 1065
Db 571 AACTCCCGGACACCCAGGAGTGGCCCTTAGAAAAAGCAAGCAAGTGTGAAAAATTATC 630
QY 1066 AGTTCCTACAAGCACACAACCTCCATCTTCGACGACTTTTGCTCAGTACGAGAGCGCCAG 1125
Db 631 AGTTCCTACAAGCACACAACCTCCATCTTCGATGACTTTTGTCTCAGTACGAGAGCGCCAG 690
QY 1126 AGAGGAGGAGGTGGTGGCCAGGAACCGCAGAGTGTGAAAAA 1168
Db 691 GACGACGAGGAAGTGGTGGCAAGGAACCGCAGAGTGTGAAAAA 733

RESULT 12
BM685329
LOCUS
DEFINITION
UI-B-C10-aab-d-01-0-UI.r1 UI-B-C10 Homo sapiens cDNA clone
UI-B-C10-aab-d-01-0-UI 5', mRNA sequence.
ACCESSION
BM685329
VERSION
BM685329.1 GI:18995225
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 633)
AUTHORS
Bonald, M.F., Lennon, G. and Soares, M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
COMMENT
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
```

QY 1743 TTTT TTTT TTTT TGAAAAATCTTTCCTTCCA 1774


```
|||||
Db 424 AATAACGACAAACACCGGTCAAAATCTCCGGGACACCCAGGAGTGCCTTTAGAAAA 365
QY 1042 GCCAAGCAAGTGTGAAAATTTATCAGTTCTTACAAGCACACAACTCTTCTTCGACGAC 1101
Db 364 GCCAAGCAAGTGTGAAAATTTATCAGTTCTTACAAGCACACAACTCTTCTTCGACGAC 305
QY 1102 TTTTGCTCATTACGAGAACGCCCA-GAGGAGGAGGAGTGTGCGAAGAACCGCAGAGT 1160
Db 304 TTTTGCTCATTACGAGAACGCCCAAGGAGGAGGAGTGTGCGAAGAACCGCAGAGT 245
QY 1161 CGAAACAAACAAATGAGGCGCAACAGTTTC-TTACATGTTCTAACGTTTACGTTTGA 1219
Db 244 CGAAACAAACAAATGAGGCGCAACAGTTTC-TTACATGTTCTAACGTTTACGTTTGA 185
QY 1220 CAGTTTAAACACGTTGCTTGTGTCAGTCCAGTGTGTCGTCGCGGGGTTGAGTG 1279
Db 184 CAGTTTAAACACGTTGCTTGTGTCAGTCCAGTGTGTCGTCGCGGGGTTGAGTG 125
QY 1280 TTGCATCTTTGCCCTTCTTGTGCTGTTGATTTTTTGGCCAGATGATCTGCATTTATTTGTAC 1339
Db 124 TTGCATCTTTGCCCTTCTTGTGCTGTTGATTTTTTGGCCAGATGATCTGCATTTATTTGTAC 65
QY 1340 TTTTCTATGATATTAATCCTCTAGAGTCACTAATAAGGAGTATTTTTTT 1393
Db 64 TTTTCTATGATATTAATCCTCTAGAGTCACTAATAAGGAGTATTTTTTT 11

RESULT 14
BG911605
LOCUS 602812729F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4944846
5', mRNA sequence.
ACCESSION BG911605
VERSION BG911605.1 GI:14292081
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 689)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10890 row: i column: 07
High quality sequence stop: 663.
Location/Qualifiers
1. .689
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 190 a 154 C 157 G 188 T
ORIGIN
```

Query Match 29.3%; Score 594.6; DB 13; Length 689;
Best Local Similarity 97.0%; Pred. No. 3.7e-117;

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Matches 670; Conservative 0; Mismatches 14; Indels 7; Gaps 6;
QY 870 CGGCACCACTGCGGGGTCTGTCTCAGCAAGTGGAGGGAGATTTTGATGTCCAGTG 929
Db 1 CGGCACCACTGCGGGGTCTGTCTCAGCAAGTGGAGGGAGATTTTGATGTCCAGTG 60
QY 930 GATTTTGTAAAGATGTACCAATTAACCAAGTCCGGCACATCAGGCTGGAGATAACGA 989
Db 61 GATTTTGTAAAGATGTACCAATTAACCAAGTCCGGCACATCAGGCTGGAGATAACGA 120
QY 990 CAACAAACCGGTCAAAAATCTCCGGGACACCCAGGAGGTGCCCTTAGAAAAAGCCAAAGCA 1049
Db 121 CAACAAACCGGTCAAAAATCTCCGGGACACCCAGGAGGTGCCCTTAGAAAAAGCCAAAGCA 180
QY 1050 AGTGTGAAAATTTATCAGTTCTTACAAGCACACAACTCCATCTTCGACGACTTTGCTCA 1109
Db 181 AGTGTGAAAATTTATCAGTTCTTACAAGCACACAACTCCATCTTCGACGACTTTGCTCA 240
QY 1110 CTACGAGAACGCCCA-GAGGAGGAGGAGTGTGCGCAAGGACCGCAGAGTCGAACAA 1168
Db 241 CTACGAGAACGCCCAAGGAGGAGGAGTGTGCGCAAGGACCGCAGAGTCGAACAA 300
QY 1169 ACAATGAGGCGCAACAGTTTCTTACATGTTCTAACGTTTGACTTTGAAAAACAGTTTAAA 1228
Db 301 ACAATGAGGCGCAACAGTTTCTTACATGTTCTAACGTTTGACTTTGAAAAACAGTTTAAA 360
QY 1229 ACACGTGTGCTTTGGTCCAGTCCAGTGTGTCGTCGCGGGGTTGAGTGTTCGATCTT 1288
Db 361 ACACGTGTGCTTTGGTCCAGTCCAGTGTGTCGTCGCGGGGTTGAGTGTTCGATCTT 420
QY 1289 TGCCTTCTTGTGCTGTTGATTTTGGCCAGATGATCTGCATTTATTTGTACTTTTCTAT 1348
Db 421 TGCCTTCTTGTGCTGTTGATTTTGGCCAGATGATCTGCATTTATTTGTACTTTTCTAT 480
QY 1349 GTATTATAATCCTGTAGAGTCACTAATAAGGAGTATTTTTTTTGTGACGCTTATCAAT 1408
Db 481 GTATTATAATCCTGTAGAGTCACTAATAAGGAGTATTTTTTTTGTGACGCTTATCAAT 538
QY 1409 CAGACTGATCTAATGTGAATGTAAAGTATCCTTTAAAAAACAAGCATCTAT-TTTGGCAGA 1467
Db 539 CAGACTGATCTAATGTGACATGTAAAGTATCCTTTAAAAAACAAGCATCTATCCTCGCAGA 598
QY 1468 AATTGTGTTCTTAAATTCAGTCAATTTGA-TATTCTGTGAGACTTCAATAT-TTCTCATCCC 1525
Db 599 AATTGTGTTCTTAAATTCAGTCAATCCTGACTATTTCTGTGACACTTCAATGCTCTCATCCC 658
QY 1526 TTTATTG-CTTTTACCAACATAAGAAC 1555
Db 659 TTTATTGCTTTTATTAGCAACATTAGAAAGC 689

RESULT 15
LOCUS AW387914/c 600 bp mRNA linear EST 04-FEB-2000
DEFINITION MR4-ST0119-071099-010-F01 ST0119 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW387914
VERSION AW387914.1 GI:6892573
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 600)
HCGP http://www.ludwig.org.br/ORESTES
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
```

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LiCR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR4&t2=MR4-ST0119-071099-010-F01&t3=1999-10-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 581.

FEATURES

Location/Qualifiers
1..600
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0119"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site: 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
124 a 169 c 151 g 156 t

BASE COUNT

ORIGIN

Query Match 28.8%; Score 583.2; DB 10; Length 600;
Best Local Similarity 99.3%; Pred. No. 1e-114;
Matches 596; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 676 ATCAAGAGCTACTCTGAGCAGCATCCACCGCTCCATTAGTACTCCATCTGTTGATGC 735
Db 600 ATCAAGAGCTACTCTGAGCAGCATCCACCGCTCCATTAGTACTCCATCTGTTGATGC 541
Qy 736 ACAGAGCAGCGCAACAGCGCTGGACAGCGCTTCCGCTGCATGAGCAGCAAGGGGCC 795
Db 540 ACAGAGCAGCGCATCAAGCGCTGGACAGCGCTTCCGCTGCATGAGCAGCAAGGGGCC 481
Qy 796 GTCTACCTGCTCTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCCGAGATGAG 855
Db 480 GTCTACCTGCTCTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCCGAGATGAG 421
Qy 856 TCCCGCTGGACTACGGCACCAGTGCAGGCTGCTGCTCAGGACACAGTGAAGGGGAAG 915
Db 420 TCCCGCTGGACTACGGCACCAGTGCAGGCTGCTGCTCAGGACACAGTGAAGGGGAAG 361
Qy 916 TTGTATGTCCAGTGGATTTTGTAAAGGATGTACCCATATACAGCTCCGCGACATCAGG 975
Db 360 TTGTATGTCCAGTGGATTTTGTAAAGGATGTACCCATATACAGCTCCGCGATCAGG 301
Qy 976 CTGAGAAATACGACAAACACCGGTACAAACTCCCGGGACACCCAGGAGTGCCTTTA 1035
Db 300 CTGAGAAATACGACAAACACCGGTACAAACTCCCGGGACACCCAGGAGTGCCTTTA 241
Qy 1036 GAAAAGCCAGCAAGTGTCTCAAAATATATAGTTTCTTACAGGACACACCTCCATCTTC 1095
Db 240 GAAAAGCCAGCAAGTGTCTCAAAATATATAGTTTCTTACAGGACACACCTCCATCTTC 181
Qy 1096 GACGACTTTGTCTACTACGAGAGCGCCA - GAGGAGGAGGAGGTGCTGCGCAAGAAACGG 1154
Db 180 GACGACTTTGTCTACTACGAGAGCGCCAAGGAGGAGGAGGTGCTGCGCAAGAAACGG 121
Qy 1155 CAGAGTGGAAACAAACATGAGGCGCAACCGATTTCTTACATGTTCTAAACGTTTGTG 1214
Db 120 CAGAGTGGAAACAAACATGAGGCGCAACCGATTTCTTACATGTTCTAAACGTTTGTG 61
Qy 1215 GAAAACAGTTTTAAACACAGTGTGCTGTGACGTCAGTCCAGTGTGCTCCCGTGGGGGTT 1274
Db 60 GAAAACAGTTTTAAACACAGTGTGCTGTGACGTCAGTCCAGTGTGCTCCCGTGGGGGTT 1

RESULT 16

BE892829 808 bp mRNA linear EST 20-OCT-2000
LOCUS 60133961F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919191 5',
DEFINITION mRNA sequence.

ACCESSION

BE892829.1 GI:103533393

VERSION

EST.

KEYWORDS

human.

SOURCE

ORGANISM

REFERENCE

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JOURNAL

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FEATURES          Location/Qualifiers
  source          1..669
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone_lib="MAGE reserenceses, MAGH"
                  /note="Vector: pluescriptSKm"
BASE COUNT       175 a 107 c 135 g 252 t
ORIGIN
Query Match      28.2%; Score 571; DB 10; Length 669;
Best Local Similarity 97.4%; Pred. No. 4.3e-112;
Matches 591; Conservative 0; Mismatches 15; Indels 1; Gaps 1;
Qy 1396 TCAGCTTATCAATCAGACTGATTAATGTGAATGTAAGTATCCTTAAACAAAGCATC 1455
Db 1 TCAGCTTATCAATCAGACTGATTAATGTGAATGTAAGTATCCTTAAACAAAGCATC 60
Qy 1456 TATTTGGCAGAAATGGTCTTAAATTCAGTCAATTTGATATCTGTGAGACTTCATAT 1515
Db 61 TATTTGGCAGAAATGGTCTTAAATTCAGTCAATTTGATATCTGTGAGACTTCATAT 120
Qy 1516 TCTCATCCCTTTATGGCTTTTGTAGCAACATAGAAACCATGAGTCAATTTGTGCAATTA 1575
Db 121 TCTCATCCCTTTATGGCTTTTGTAGCAACATAGAAACCATGAGTCAATTTGTGCAATTA 180
Qy 1576 GAGTATTCGTAAATCTCTTGAATACTGAAATCAAAAGGTTAATGATTTTGTTC 1635
Db 181 GAGTATTCGTAAATCTCTTGAATACTGAAATCAAAAGGTTAATGATTTTGTTC 240
Qy 1636 ATTCGATTTGCTATTTATATCTGTTATCGGTCTAAAGTCTAAATTTACCCATTTGAT 1695
Db 241 ATTCGATTTGCTATTTATATCTGTTATCGGTCTAAAGTCTAAATTTACCCATTTGAT 300
Qy 1696 TTTTCTGCTAGACAGATAACTTTTAAATTTTCAAAATTTGGCAGACAC-TTTTTTTTTT 1754
Db 301 TTTTCTGCTAGACAGATAACTTTTAAATTTTCAAAATTTGGCAGACACTTTTTTTTTT 360
Qy 1755 TTTGAAATCTTTCTCCAGATCTGTTGCCACTGAAACAGCCACCCCTCCCTCACTGTC 1814
Db 361 TTTGAAATCTTTCTCCAGATCTGTTGCCACTGAAACAGCCACCCCTCCCTCACTGTC 420
Qy 1815 CTGGTGTCCGATTTGGCTGGATGTTGGGGCATGATGTGTGAGGAACTGGAAGGTGC 1874
Db 421 CTGGTGTCCGATTTGGCTGGATGTTGGGGCATGATGTGTGAGGAACTGGAAGGTGC 480
Qy 1875 TTTAGGTCGTGTCAGGTCGGGCATCTTTGTTGTTTGGACATCTTTTAAATTTTACA 1934
Db 481 TTTAGGTCGTGTCAGGTCGGGCATCTTTGTTGTTTGGACATCTTTTAAATTTTACA 540
Qy 1935 CCTTTTCTTAAGAAATCTTAATGCCGCTCTTAAGTTTATACCAATAATGCTGAGCTTTAA 1994
Db 541 CCTGTTTCAAGAAATCTTAATGCCAGTTTATAGTTGTTATACCAATAATGCTGAGCTTTA 600
Qy 1995 GTGTAGG 2001
Db 601 ATGGTGG 607

RESULT 19
BI262492/c
LOCUS
DEFINITION 602953767T1 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:508792 3',
mRNA sequence.
ACCESSION BI262492
VERSION BI262492.1 GI:14822752
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 582).
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
```

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Dr. Louis Staudt, M.D., Ph.D. cDNA Library
Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLCMI846 row: e column: 17
High quality sequence start: 27
High quality sequence stop: 580.

FEATURES

source

1..582
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcORI; cDNA made by oligo-dT priming. Directionally cloned
into EcORI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT 142 a 161 c 133 g 146 t
ORIGIN

Query Match 27.4%; Score 555; DB 13; Length 582;

Best Local Similarity 99.0%; Pred. No. 1.2e-108;

Matches 569; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 779 TGACGACAGAGGGCCGCTCTACCTGCTCTTACGCGTCAATGGGAGTGGGCATTTTGTG 838

Db 582 TGACGACAGAGGGCCGCTCTACCTGCTCTTACGCGTCAATGGGAGTGGGCATTTTGTG 523

Qy 839 GGGTGGCCGAGATGAATGCCCGCTGACGTACGGCACAGTGCCTGGGGTCTGGTCTCAGG 898

Db 522 GGGTGGCCGAGATGAATGCCCGCTGACGTACGGCACAGTGCCTGGGGTCTGGTCTCAGG 463

Qy 899 ACAAGTGGAGGGGAAGTTGATGTCAGTGGATTTTGTAAAGATGTACCCAAATACC 958

Db 462 ACAAGTGGAGGGGAAGTTGATGTCAGTGGATTTTGTAAAGATGTACCCAAATACC 403

Qy 959 AGCTCCGGCACATCAGGCTGGAGAAATACGACAAACAAACCGGTCAAACTCCCGGGACA 1018

Db 402 AGCTCCGGCACATCAGGCTGGAGAAATACGACAAACAAACCGGTCAAACTCCCGGGACA 343

Qy 1019 CCCAGGAGTGGCCCTTAGAAAAAGCCAAAGCAAGTGTGAAAAATATCAGTTCCTACAGC 1078

Db 342 CCCAGGAGTGGCCCTTAGAAAAAGCCAAAGCAAGTGTGAAAAATATCAGTTCCTACAGC 283

Qy 1079 ACACAACTCCATCTTCGACGACTTTGCTCACTACGAGAGCGCCA-GAGGAGGAGG 1137

Db 282 ACACAACTCCATCTTCGACGACTTTGCTCACTACGAGAGCGCCA-GAGGAGGAGG 223

Qy 1138 TGGTGCACAAGGAACGCGCAGAGTCGAAACAAACAAATGAGGCGCAACAGTTTCTTACATG 1197

Db 222 TGGTGCACAAGGAACGCGCAGAGTCGAAACAAACAAATGAGGCGCAACAGTTTCTTACATG 163

Qy 1198 TTTCAAGCTTTGACTTTGAAAAAAGAGTTTAAAAACAGTGTGCTGGTCCAGTCCAGTGTGT 1257

Db 162 TTTCAAGCTTTGACTTTGAAAAAAGAGTTTAAAAACAGTGTGCTGGTCCAGTCCAGTGTGT 103

Qy 1258 CGTCCCGTGGGGGTTGAGTGTGTCATCTTTCGCTTTCTGCTGTTGATTTTGGCCAG 1317

Db 102 CGTCCCGTGGGGGTTGAGTGTGTCATCTTTCGCTTTCTGCTGTTGATTTTGGCCAG 43


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low stringency conditions."
BASE COUNT      116 a   161 c   139 g   147 t
ORIGIN
Query Match      27.2%; Score 551; DB 10; Length 563;
Best Local Similarity 99.8%; Pred. No. 8.4e-108;
Matches 562; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 713 TTAAGTACTCCATCTGGTGTAGCAGACGCGCAACAGCGCTGGACAGCCCTTCC 772
DB 563 TTAAGTACTCCATCTGGTGTAGCAGACGCGCAACAGCGCTGGACAGCCCTTCC 504
QY 773 GCTCATGAGCAGCAGAGGGGCGCTTACCTGCTTTCAGCGTCAATGGGAGTGGCATT 832
DB 503 GCTCATGAGCAGCAGAGGGGCGCTTACCTGCTTTCAGCGTCAATGGGAGTGGCATT 444
QY 833 TTTGTGGGTCGCGCAGATGAAGTCCCGGTGGACTACGGCACCAGTGCAGGGTCTGGT 892
DB 443 TTTGTGGGTCGCGCAGATGAAGTCCCGGTGGACTACGGCACCAGTGCAGGGTCTGGT 384
QY 893 CTCAGGCAAGTGAAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGGATGTACCCA 952
DB 383 CTCAGGCAAGTGAAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGGATGTACCCA 324
QY 953 ATACCCAGCTCCGCGACATCAGGCTGGAGATTAAGCAACAACCCGTCACAACTCCC 1012
DB 323 ATACCCAGCTCCGCGACATCAGGCTGGAGATTAAGCAACAACCCGTCACAACTCCC 264
QY 1013 GGGACACCCAGAGTGCCCTTAGAAAAGCCAAAGCAAGTCTGAAAATTATCATGTTCT 1072
DB 263 GGGACACCCAGAGTGCCCTTAGAAAAGCCAAAGCAAGTCTGAAAATTATCATGTTCT 204
QY 1073 ACAAGCACACACCTCCATCTTCGACGACTTGTCTACTACGAGAAGGCCA-GAGGAG 1131
DB 203 ACAAGCACACACCTCCATCTTCGACGACTTGTCTACTACGAGAAGGCCA-GAGGAG 144
QY 1132 AGGAGTGTGCGCAGAGCAGGAGTGCAGCAACAACAATAGGCGCAACCACTTCT 1191
DB 143 AGGAGTGTGCGCAGAGCAGGAGTGCAGCAACAACAATAGGCGCAACCACTTCT 84
QY 1192 TACATGTTCTAAAGTTCGACTTTGAAAACAGTTTAAAACAGTGTGCTGAGTCCCA 1251
DB 83 TACATGTTCTAAAGTTCGACTTTGAAAACAGTTTAAAACAGTGTGCTGAGTCCCA 24
QY 1252 GTGTGTCGTCCTCCGTCGGGGGTT 1274
DB 23 GTGTGTCGTCCTCCGTCGGGGGTT 1

RESULT 22
BG216572 LOCUS      BG216572      893 bp      mRNA      linear      EST 21-APR-2001
DEFINITION RST36264 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG216572
VERSION     BG216572.1 GI:13742593
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 893)
AUTHORS   Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
            Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
            Creation of genome-wide protein expression libraries using random
            activation of gene expression
            Nat. Biotechnol. 19 (5), 440-445 (2001)
            2127151
COMMENT    Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
```

BM014798 688 bp mRNA linear EST 30-OCT-2001
LOCUS 603640668F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5416745 5',
DEFINITION mRNA sequence.
ACCESSION BM014798.1 GI:16529152
VERSION BM014798
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 688)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLMI2063 row: g column: 18
High quality sequence stop: 679.
Location/Qualifiers
FEATURES
source
1..688
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5416745"
/clone_lib="NIH MGC 87"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: breast; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
BASE COUNT 174 a 118 c 140 g 256 t
ORIGIN
Query Match 26.8%; Score 542.8; DB 13; Length 688;
Best Local Similarity 94.8%; Pred. No. 4.7e-106;
Matches 626; Conservative 0; Mismatches 27; Indels 7; Gaps 6;
QY 1374 AATAAGGAGTATTTTGTGTCAGCTTATCAATCAGACTGATCTAATGTGAATCTAA 1433
DB 1 AATAAGGAGTA-TTTTTTGTGTCAGCTTATCAATCAGACTGATCTAATGTGAATCTAA 59
QY 1434 GTATCCTTAAAAACAAGCATCTATTTGGCAGAAATGTGTTCTTAAATTCAGTCAATTT 1493
DB 60 GTATCCTTAAAAACAAGCATCTATTTGGCAGAAATGTG-TCTTAAATTCAGTCAATTT 118
QY 1494 GATATTCGTGAGACTTCATATTTCTCATCCCTTATTTGCTTTTGTAGCAACATAAGAAA 1553
DB 119 GATATTCGTGAGACTTCATATTTCTCATCCCTTATTTGCTTTTGTAGCAACATAAGAAA 178
QY 1554 CCATGAGTCATTTTGTCAATTTAGAGTATCTGATAAATCTCTGAAATCTGAATCA 1613
DB 179 CCATGAGTCATTTTGTCAATTTAGAGTATCTGATAAATCTCTGAAATCTGAATCA 238
QY 1614 AAGGTTAATCATTTTGTTCATTCGATTTGTTCATTTTATTCGTTATCGGTCTAA 1673
DB 239 AAGGTTAATCATTTTGTTCATTCGATTTGTTCATTTTATTCGTTATTCGTTCTAA 298
QY 1674 AGTGCTAATTTACCCATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTT 1733
DB 299 AGTGCTAATTTACCCATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTT 358
QY 1734 GGCAGACACTTTTTTTTTT-TTTTGAATAATCTTTCCCTTCAGATCTGTTGCCCACTGAA 1792
DB 359 GGCAGACACTTTTTTTTTTCTTTGGAAATCTTTTCTTCCAGATCTGTGGCCCACTGAA 418

QY 1793 CAGCCACCCGTCCTCCTCCTCCTGCTGTCCTGATGGGCTGGATGCTGTTGGGGCATGAT 1852
DB 419 CAGCCACCCGTCCTCCTCCTCCTGCTGTCCTGATGGGCTGGATGCTGTTGGGGCATGAT 478
QY 1853 GTGTGGAGGAACCTGGAAGGTGCTTTTAGGTCTGTTTCAGGCTCGGGCATCTTTGTTG--T 1910
DB 479 GTGTGGAGGACACTGGAAGGTGCTTAGGTCTGTTTCAGGCTCGGGCATCTTTGTTGTC 538
QY 1911 TTGCACATCTTTTAAATTTTACACCTTTTCTTAAGAAATCTTAATCCGCTTTAAAGTTT 1970
DB 539 TTGCACATCTTTTGAATTTTACACCTTTTCTTAAGAAATCTTAATCCGCTTTAAAGTTT 598
QY 1971 TATACCAATAAGTCTGAGCTTTTAAAG-TGTAGAT-CTGTAGTACAGACAGTGTGATGA 2028
DB 599 TATCCCAATAAGTCTGAGCTTTTAAAGCTGTAGGATCCGGGTAGTACAGACAGTGTGATGA 658
RESULT 24
BE542593 837 bp mRNA linear EST 09-AUG-2000
LOCUS 601063983F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450261 5',
DEFINITION mRNA sequence.
ACCESSION BE542593
VERSION BE542593.1 GI:9771238
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 837)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ARCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8428 row: f column: 22
High quality sequence stop: 631.
Location/Qualifiers
FEATURES
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3450261"
/clone_lib="NIH MGC 10"
/cell_line="MGC36"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
BASE COUNT 193 a 231 c 252 g 161 t
ORIGIN
Query Match 25.6%; Score 519.2; DB 10; Length 837;
Best Local Similarity 92.8%; Pred. No. 5.3e-101;
Matches 655; Conservative 0; Mismatches 38; Indels 13; Gaps 10;
QY 577 AGCGTCGAATCCCAACCCCGCTCTTGAATAACTGAAGCTCTCACAGCTACACCCGAAA 636
DB 1 AGCGTCGAATCCCAACCCCGCTCTTGAATAACTGAAGCTCTCACAGCTACACCCGAAA 60
QY 637 GAGTTTGTAGTGGAAATCTGAAAGCGGCGGTGTGTTCAT-CATCAAGAGTACTCTGAGGA 695
DB 61 GAG-TTGTAGTGGAAATCTGAAAGCGGCGGTGTGTTCATCCATCAAGAGTACTCTGAGGA 119
QY 696 CGACATCCACCG-CTCCATTTAAGTACTCTCCATCTGTGTGTAGCAGACAGCGCAACAGC 754

Db	120	CGAATCACCAGCCCTCCATTAAAGTACTCCATCTGGTGTAGCACAGACCGCAACAAGC	179
Qy	755	GCCTGGACAGAGCCCTTCCGC - TGCATGAGCAGCAAGAGGCGCCGTCTACTGCTCTTCAAGC	813
Db	180	GCCTGGACAGAGCCCTTCCGCCTGCATGAGCAGCAAGAGGCGCCGTCTACTGCTCTTCAAGC	239
Qy	814	GTCAATGGAGTGGGCATTTTTTGTGGGTGGCCGAGATGAAGTCCCCCGTGGACTACGGC	873
Db	240	GTCAATGGAGTGGGCAT - TTTTGTGGGTGGCCGAGATGAAGTCCCCCGT - GACTACGGC	297
Qy	874	ACCAAGTCCCGGGTCTGGTCTCAGGACAGTGGAGGGGAAGTTTGATGTCAGTGGATT	933
Db	298	ACCAAGTCCCGGGTCTGGTCTCAGGACAGTGGAGGGGAAGTTTGATGTCAGTGGGA - T	356
Qy	934	TTTGTAAAGGATGTACCCCAATAACAGAGCTCCGGCACATCAGGCTGGAGAAATAACGACAAC	993
Db	357	TTTGTAAAGGATGTACCCCAATAACAGAGCTCCGGCACATCAGGCTGGAGAAATAACGACAAC	416
Qy	994	AAACCGGTCACAAACTCCCGGACACCCAGAGGTGCCCTTAGAAAAAGCCAAAGCAAGTG	1053
Db	417	AAACCGGTCACAAACTCCCGGACACCCAGAGGTGCCCTTAGAAAAAGCCAAAGCAAGTG	476
Qy	1054	CTGAATATTATCAGTTCTTACAGCACACACCTCCATCTTCGAGAGCTTTGCTCACTAC	1113
Db	477	CTGAATATTATCAGTTCTTACAGCACACACCTCCATCTTCGAGAGCTTTGCTCACTAC	536
Qy	1114	GAGAGGCGCAG - AGGAGGAGGAGGTGGTCCGCAAGGAAGCGAGAGTCCAAACAACA	1171
Db	537	GAGAGGCGCAGGAGGAGGAGGAGGTGGTCCGC - AGGAGCGGAGAGTGCACACAATAC	595
Qy	1172	ATGAGGGCGAACCAAGTTTCTTACATGTTCTTAACGTTTGACTTTGAAAAACAGTTTAAACA	1231
Db	596	AATGGGGGACCAAGTCTCTTACATGTTCTTAACGTTTGACTTT - GAAACGTTTAAACCC	652
Qy	1232	CGTGTGCTTGCTAGCTCCAGTGTGCTCCGTCGCGGGGGTTGAG	1277
Db	653	CGTGTGCTGCTCCGCTCCAGTGTGCTCCGCGGGGGTGGGTG	698

RESULT 25

AL562740/c

LOCUS

DEFINITION

AL562740 LTI_NFL003_NBC3 Homo sapiens mRNA linear EST 16-FEB-2001

prime, mRNA sequence.

ACCESSION

AL562740

VERSION

GI:12911458

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 921)

AUTHORS

Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

Location/Qualifiers

1..921

source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DC020YI04"

/clone_lib="LTI_NFL003_NBC3"

/sex="male"

/tissue_types="neuroblastoma cells"

/lab_host="DH10B"

/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6"

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 REVERSE.

FEATURES

Source

Location/Qualifiers

1..598

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="UI-E-EJ1-a19-a-05-0-UI"

/clone_lib="UI-E-EJ1"

/tissue_type="fetal eyes, lens, eye anterior segment,

optic nerve, retina, Retina Foveal and Macular, RPE and

Choroid"

/dev_stage="fetal and adult"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

UI-E-EJ1 is a subcloned cDNA library constructed

according to Bonaldo, Lennon and Soares, Genome Research,

6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double

stranded cDNA was ligated to an EcoR I adaptor, digested

with Not I, and cloned directionally into pT7T3-Pac

vector. The oligonucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is

located between the Not I site and the (dT)18 tail. The

sequence tags for this library are: fetal eyes, AGAATCAAGA

; lens, CGATTAGGCA; eye anterior segment, AATGCCGCAAT;

optic nerve, CCATTAGGTC; retina, CCGCG; Retina Foveal and

Macular, GTCC; RPE and Choroid, ACCTA. This library was

created for the program, Gene Discovery in the Visual

System, supported by National Eye Institute (NEI)."

146 a 99 c 117 g 236 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 25.2%; Score 512; DB 14; Length 598;

Matches 523; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1505 AGACTTCATATTTCTCATCCCTTATTGCTTTTATAGCAACATAAGAAACCATGAGTCAT 1564

Db 1 AGACTTCATATTTCTCATCCCTTATTGCTTTTATAGCAACATAAGAAACCATGAGTCAT 60

QY 1565 TTGTGCTATTTAGAGTATCTGATAAAATCTCTTGAATAATCTGAATCAAAAGGTTAATG 1624

Db 61 TTGTGCTATTTAGAGTATCTGATAAAATCTCTTGAATAATCTGAATCAAAAGGTTAATG 120

QY 1625 ATTTTGTGTCATCTGATTTGTCATTTTATATATCTGTTATCGGTCTAAAGTCTAATTT 1684

Db 121 ATTTTGTGTCATCTGATTTGTCATTTTATATATCTGTTATCGGTCTAAAGTCTAATTT 179

QY 1685 ACCATTGTGATTTTTCGCTAGACAGATACTTTTAAATTTTCAAATTTGCGCAGACACTT 1744

Db 180 ACCATTGTGATTTTTCGCTAGACAGATACTTTTAAATTTTCAAATTTGCGCAGACACTT 239

QY 1745 TTTTGTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGATTTT 1804

Db 240 TTTTGTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGATTTT 299

QY 1805 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1864

Db 300 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359

QY 1865 TGGAGGTGCTTTTAGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1924

Db 360 TGGAGGTGCTTTTAGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419

QY 1925 AAATTTTACACCTTTTCTTAAGAAATCTTAATGCGGTCTTAAGTTTATACCAATAATGC 1984

Db 420 AAATTTTACACCTTTTCTTAAGAAATCTTAATGCGGTCTTAAGTTTATACCAATAATGC 479

QY 1985 TGAGCTTTAAAGTGTAGGATCTCGTAGTACAGACAGTGTGATGGA 2028

Db 480 TGAGCTTTAAAGTGTAGGATCTCGTAGTACAGACAGTGTGATGGA 523

RESULT 27

BG828010

LOCUS

DEFINITION

ACCESSION

KEYWORDS

SOURCE

ORGANISM

COMMENT

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..886

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4905060"

/clone_lib="NIH MGC 17"

/tissue_type="thalamocortical"

/lab_host="DH10B (phage-resistant)"

/note="Organ: muscle; Vector: pOTB7; Site 1: EcoRI;

Site 2: XhoI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

229 a 258 c 220 g 179 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 25.0%; Score 506.2; DB 12; Length 886;

Matches 563; Conservative 0; Mismatches 18; Indels 6; Gaps 4;

QY 595 GTCTTTGAAAACCTGAGGCTGCTCAGCTACACCCGAAAGAGTTTGAGTGGATCTG 654

Db 2 GTCTTTGAAAACCTGAGGCTGCTCAGCTACACCCGAAAGAGTTTGAGTGGATCTG 61

QY 655 AAAAGCGGGGTGTGTTCATCATCAAGAGCTACTCTGAGGACGACATCCACCGCTCCATT 714

Db 62 AAAAGCGGGGTGTGTTCATCATCAAGAGCTACTCTGAGGACGACATCCACCGCTCCATT 121

QY 715 AAGTACTCCATCTGTTGTAGCAGACGCGCAACAAGCGCTTGACAGCGCTTCCCG 774

Db 122 AAGTACTCCATCTGTTGTAGCAGACGCGCAACAAGCGCTTGACAGCGCTTCCCG 181

QY 775 TGATGAGCAGCAGAGGGGGCCGCTCTACCTGCTCTTTCAGCGTCAATGGGAGTGGGCAATTTT 834

Db 182 TGATGAGCAGCAGAGGGGGCCGCTCTACCTGCTCTTTCAGCGTCAATGGGAGTGGGCAATTTT 241

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Qy 835 TGTGGGTGGCGAGATGAAGTCCCTGGAATACGCAACAGTCCCGGGTCTGGTCT 894
Db 242 TGTGGGTGGCGAGATGAAGTCCCTGGAATACGCAACAGTCCCGGGTCTGGTCT 301
Qy 895 CAGCAAGTGGAGGGGAAGTTGATGCTCAGTGGATT--TTGTTAAGGATGTACCCA 952
Db 302 CAGCAAGTGGAGGGGAAGTCTGATGCTCAGTGGATT--TTGTTAAGGATGTACCCA 361
Qy 953 ATAACCACTCCGCGACATCAGGCTGGAGAAATACGCAACAAACCGGTACAAACTCCC 1012
Db 362 ATAACCACTCCGCGACATCAGGCTGGAGAAATACGCAACAAACCGGTACAAACTCCC 421
Qy 1013 GGGACACCAGAGGTGCCCTTAG--AAAAAGCCCAAGTGTCTGAAATTTATCAGTTC 1070
Db 422 GGGACACCAGAGGTGCCCTTAGCAAAACAAAGCAAGCAAGTGTCTGAAATTTATCAGTTC 481
Qy 1071 CTACAGCACACCACTTCATCTCGAGACTTTGCTCACTACGAGAGCGCCA-GAGGA 1129
Db 482 CTACAGCACACCACTTCATCTCGAGACTTTGCTCACTACGAGAGCGCGAGGAGGA 541
Qy 1130 GGAGGAGTGTG-CGCAAGGAACGGCAGAGTCCGAAACAAATGA 1175
Db 542 GGAGGAGTGTGCGCGAAGGAACGGCGCAGCTCGCAACACCAAGA 588

RESULT 28
LOCUS AW387819 659 bp mRNA linear EST 04-FEB-2000
DEFINITION MR4-ST0118-021299-021-a06 ST0118 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW387819
VERSION AW387819.1 GI:6892478
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 659)
AUTHORS HCSP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&st2=MR4-ST0118-021299-021-a06&st3=1999-12-02&st4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 658.
FEATURES
source 1..659
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0118"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 178 a 175 c 179 g 127 t
ORIGIN

```

Query Match

24.8%; Score 503.6; DB 10; Length 659;

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Best Local Similarity 95.8%; Pred. No. 1.2e-97;
Matches 571; Conservative 0; Mismatches 19; Indels 6; Gaps 5;

Qy 559 CAGCTTAATTTCTGCCCCCAGCGTCGAATCCACCCCGTCTTTGAAAAACGAAAGCGTCT 618
Db 22 CAGCTTAATTTCTG--CCAGGTCGAATCCACCCCGTCTTTGAAAACTGAAGCGTCTC 79
Qy 619 CACAGCTACAAACCCGAAAGAGTTTGAAGTGGAAATCTGAAAA--GCGGGGGTGTGTTTCATCAT 677
Db 80 ACAGGCTACAAACCCGAAAGAGTTTGAATGGAATCTGAAAAAGCGGGCGTGTGTTTCATCAT 139
Qy 678 CAA-GAGCTACTCTGAGAGCAGCATCCACCGCTCCATTAAGTACTCTGTTGTAGCA 736
Db 140 CAATGAGCTACTCTGAGAGCAGCATCCACCGCTCCATTAAGTACTCTGTTGTAGCA 199
Qy 737 CAGAGCAGCGCAACAGCGCTGGACAGCGCTTCCGCTGTCATGAGCAAGAGGGGCCG 796
Db 200 CAGAGCAGCGCAACAGCGCTGGACAGCGCTTCCGCTGTCATGAGCAAGAGGGGCCG 259
Qy 797 TCTACCTGCTCTTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGGTGGCGGAGTGAAGT 856
Db 260 TCTACCTGCTCTTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGGTGGCGGAGTGAAGT 319
Qy 857 CCCCCTGGACTACGGCACCAGTGCC--GGGGTCTGGTCTCAGGACAAGTGGAGGGGAAG 915
Db 320 CCCCCTGGACTACGGCACCAGTGCCGGGGGTCTGGTCTCAGGACAAGTGGAGGGGAAG 379
Qy 916 TTTGATCTCCAGTGGATTTTGTAAAGATGTACCC--AATAACCCAGTCCCGGCACATCAG 974
Db 380 TTTGATCTCCAGTGGATTTTGTAAAGATGTACCCAAATAACAGCTCCAGCAATCAG 439
Qy 975 GCTGGAGATAACGACAAACAAACCGGTACAAACTCCCGGGACACCCAGGAGTGGCCCTT 1034
Db 440 GCTGGAGATAACGACAAACAAACCGGTACAAACTCCCGGGACACCCAGGAGTGGCCCTT 499
Qy 1035 AGAAAAAGCCAAAGTGTCTGAAAAATATATCAGTTCTCTACAGCACAACACCTCTCATCTT 1094
Db 500 AGAAAAAGCCAAAGTGTCTGAAAAATATATCAGTTCTCTACAGCACAACACCTCTCATCTT 559
Qy 1095 CGAGCACTTTGCTCACTACGAGAGCGCCAGAGGAGGAGTGGTGGCCCAAGGA 1150
Db 560 CGAGCACTTTGCTCACTACGAGAGCGCCAGAGGAGGAGTGGTGGCCCAAGGA 615

RESULT 29
LOCUS BF915645/c 530 bp mRNA linear EST 18-JAN-2001
DEFINITION IL3-UT0114-061200-373-C06 UT0114 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF915645
VERSION BF915645.1 GI:12307103
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 530)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

```

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-061200-373-C06&t3=2000-12-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 221.

FEATURES

Location/Qualifiers
1..530
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UT0114"
/dev_stage="Adult"

/notes="Organ: uterus tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 124 a 145 c 125 g 135 t 1 others

ORIGIN

Query Match 24.8%; Score 502.6; DB 12; Length 530;
Best Local Similarity 97.9%; Pred. No. 2e-97;
Matches 519; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
QY 787 AAGGGGCGCTTACCTGCTCTTACAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCC 846
Db 530 AAGGGGCGCTTACCTGCTCTTACAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCC 471
QY 847 GAGATGAAGTCCCGCGGACTACGGCACCAAGTCCCGGGTCTGGTCTCAGGACAACTGG 906
Db 470 GAGATGAAGTCCCGCGGACTACGGCACCAAGTCCCGGGTCTGGTCTCAGGACAACTGG 411
QY 907 AAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGATGTACCCATAACCACTCCGG 966
Db 410 AAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGATGTACCCATAACCACTCCGG 351
QY 967 CACATCAGGCTGGAGATACGACAAACACCGGTCACTCACTCCCGGACACCCAGGAG 1026
Db 350 CACATCAGGCTGGAGATACGACAAACACCGGTCACTCACTCCCGGACACCCAGGAG 291
QY 1027 GTGCCCTTAGAAAAAGCAAGTGTGAAATATTCAGTTCTCTCAAGCACACAACC 1086
Db 290 GTGCCCTTAGAAAAAGCAAGTGTGAAATATTCAGTTCTCTCAAGCACACCACCC 231
QY 1087 TCCATCTTCGACGACTTTGCTCACTACGAGAACGCCAG - AGGAGGAGGAGTGGTCGC 1145
Db 230 TCCATCTTCGACGACTTTGCTCACTACAAAAAGCCGACAGAAAGAGAGTGGTCGC 171
QY 1146 AAGGAAAGGAGAGTCGAAACAAATAGGGGCAACAGTTTCTTACATGTTCTAAGC 1205
Db 170 AAGGAAAGGAGAGTCGAAACAAATAGGGGCAACAGTTTCTTACATGTTCTAAGC 111
QY 1206 TTTCACTTTGAAAACAGTTTAAACACGTGTCTTGTGTCAGTCCAGTGTGTCGTCGGT 1265
Db 110 TTTGACTTTGAACACAGTTTAAACACGTGTCTTGTGTCAGTCCAGTGTGTCGTCGGT 51
QY 1266 GCGGGGGTTGAGTGTGATCTTTTGCCTTTCTTGTGCTGTTGATTTTGGCC 1315
Db 50 GCGGGGGTTGAGTGTGATCTTTTGCCTTTCTTGTGCTGTTGATTTTGGCC 1

RESULT 30
AW387869/c 551 bp mRNA linear EST 04-FEB-2000
LOCUS
DEFINITION M94-ST0118-151299-023-d10 ST0118 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW387869
VERSION AW387869.1 GI:6892528
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 551)

HCSP http://www.ludwig.org.br/ORESTES.

The FAPESP/LICR Human Cancer Genome Project

Unpublished (1999)

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=M94&t2=M94-ST0118-

151299-023-d10&t3=1999-12-15&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence stop: 484.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="ST0118"

/dev_stage="Adult"

/notes="Organ: stomach; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT 111 a 155 c 143 g 142 t

ORIGIN

Query Match 23.8%; Score 483.6; DB 10; Length 551;
Best Local Similarity 96.8%; Pred. No. 2.4e-93;
Matches 536; Conservative 0; Mismatches 14; Indels 4; Gaps 4;
QY 716 AGTACTCCATCTGGTGTAGCACAGACGCGCAACAGCGCCTTGACAGCGCTTCCGCT 775
Db 551 AGTACTCCATCTGGT-TAGCACAGACGCGCAACAGCGCCTTCCGCT 494
QY 776 GCATGACGACGAGGGCGCGCTCTACTGCTCTTACGCGTCAATGGAGTGGCATTTT 835
Db 493 GCATGACGACGAGGGCGCGCTCTACTGCTCTTACGCGTCAATGGAGTGGCATTTT 434
QY 836 GTGGGGTGGCGGAGATGAAGTCCCGCTGGACTACGCGCACCGAGTCCGCGGTCTGGTCTC 895
Db 433 CTGGGGTGGCGGAGATGAAG-CCCGCTGGACTACGCGCACCGAGTCCGCGGTCTGGTCTC 375
QY 896 AGGACAAGTGGAAAGGGGAAGTTTGTATGTCCAGTGGATTTTGTAAAGATGTACCCAATA 955
Db 374 AGGACAAGTGGAAAGGGGAAGTTTGTATGTCCAGTGGATTTTGTAAAGATGTACCCAATA 315
QY 956 ACCAGTCCCGGCACATCAGGCTGGAGNATACGACACAAACCGGTCCAAACCTCCCGGG 1015
Db 314 ACCAGTCCCGGCACATCAGGCTGGAGNATACGACACAAACCGGTCCAAACCTCCCGGG 255
QY 1016 ACACCCAGGAGGTGCCCTTAGAAAAAGCCAAAGCAAGTGTGAAATATTCAGTTTCTTACA 1075
Db 254 ACACCCAGGAGGTGCCCTTAGAAAAAGCCAAAGCAAGTGTGCAATTTATCGTTTCTTACA 195
QY 1076 AGCACACAACCTCCATCTTCGACGACTTTTCTCCTACGAGAAAGCGCCA-GAGGAGGAGG 1134
Db 194 AGCACACAACCTCCATCTTCGACGACTTTTCTCCTACGAGAAAGCGCCAGGAGGAGG 135
QY 1135 AGTGGTGGCGAAGGAACGCGCAGAGTTCGAACAAACAAATGAGGGCGCAACCACTTCTTAC 1194
Db 134 AGTGGTGGCGAAGGAACGCGCAGAGTTCGAACAAACAAATGAGGGCGCAACCACTTCTTAC 75


```
Db 499 CATGAGCAGCAAGGGCCGCTCTACCTGCTCTTACGCGTCAATGGAGTGGGCATTTTG 440
Qy 837 TGGGGTGGCCGAGTCAAGTCCCGCTGGACTACGGCACCAGTCCGGGTCTGGTCTCA 896
Db 439 TGGGGTGGCCGAGTCAAGTCCCGCTGGACTACGGCACCAGTCCGGGTCTGGTCTCA 380
Qy 897 GGAAGAAGTGAAGGGGAAGTTGATGTCAGTGGATTTTGTAAAGATGTACCCCAATAA 956
Db 379 GGACAAGTGAAGGGGAAGTTGATGTCAGTGGATTTTGTAAAGATGTACCCCAATAA 320
Qy 957 CAGCTCCGGCAGTCAAGTGGAGATACGACCAACACCGGTCAACAACTCCCGGGA 1016
Db 319 CCAGCTCCAGCAGTCAAGTGGAGATACGACCAACACCGGTCAACAACTCCCGGGA 260
Qy 1017 CACCCAGGAGTCCCTTAGAAAAAGCCAGCAAGTGTGAAAAATATCAGTTCCTACAA 1076
Db 259 CACCCAGGAGTCCCTTAGAAAAAGCCAGCAAGTGTGAAAAATATCAGTTCCTACAA 200
Qy 1077 GCACAACTCCATCTTCGACGACTTGTCTACTAGGAGAGCGCA-GAGGAGGAGGA 1135
Db 199 GCACAACTCCATCTTCGACGACTTGTCTACTAGGAGAGCGCA-GAGGAGGAGGA 140
Qy 1136 GTGTGTGGCAAGGACGGCAGAGTGAACAAACATGAGGGCGAACCGATTCCTTACA 1195
Db 139 GTGTGTGGCAAGGACGGCAGAGTGAACAAACATGAGGGCGAACCGATTCCTTACA 80
Qy 1196 TGTCTTAACGTTTGAAGTTCGAAACAGTTTAAACACAGTGTCTGTCAGTCCAGTGT 1255
Db 79 TGTCTTAACGTTTGAAGTTCGAAACAGTTTAAACACAGTGTGTAAGTGTGAGTCCAGTGT 20
Qy 1256 GTGTGTGGCGGGGGT 1274
Db 19 GTGTGTGGCGGGGT 1

RESULT 33
A0564196/c
LOCUS
DEFINITION HS 5363 A2 G07 T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=939 Col=14 Row=M, DNA sequence.
ACCESSION A0564196
VERSION A0564196.1 GI:4923667
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 538)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 939 row: M column: 14
Seq primer: T7
Class: BAC ends
High quality sequence stop: 538.
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FEATURES
source
Location/Qualifiers
1..538
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/db_xref="taxon:9606"
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/sex="male"
/note="vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
BASE COUNT 210 a 95 c 92 g 138 t 3 others
ORIGIN
Query Match 23.7%; Score 480.4; DB 17; Length 538;
Best Local Similarity 97.2%; Pred. No. 1.2e-92;
Matches 487; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1439 CTTAAACAAAGCATCTATTTTGGCAGAAATGTGTTCTTAAATTCAGTCATTTGATAT 1498
Db 532 CTTTAAACAAAGGCATCTATTTTGGCAGAAATGTGTTCTTAAATTCAGTCATTTGATAT 473
Qy 1499 TCTGTGAGACTTCATATTTCTCATCCCTTATTTGCTTTTACCAACATAAGAACCATG 1558
Db 472 TCTGTGAGACTTCATATTTCTCATCCCTTATTTGCTTTTACCAACATAAGAACCATG 413
Qy 1559 AGTCATTTTGTCAATTTAGAGTATCTGATAAAATCTCTTGAATACTCAAAATCAAAAGG 1618
Db 412 AGTCATTTTGTCAATTTAGAGTATCTGATAAAATCTCTTGAATACTCAAAATCAAAAGG 353
Qy 1619 TTAATGATTTTGTTCATTTCTGATTTGTTCATTTTATTAATCTGTTATCGGTCTAAAGTGC 1678
Db 352 TTAATGATTTTGTTCATTTCTGATTTGTTCATTTTATTAATCTGTTATCGGTCTAAAGTGC 293
Qy 1679 TAATTTACCCATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAG 1738
Db 292 TAATTTACCCATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAG 233
Qy 1739 ACATTTTCTTTTGTGAAAAATCTTCCCTTCCAGATCTGTTGCCACTGAACAGCCA 1798
Db 232 ACATTTTCTTTTGTGAAAAATCTTCCCTTCCAGATCTGTTGCCACTGAACAGCCA 173
Qy 1799 CCGGTCCCTCACTGTCCTGGTGTCCGATTTGGGCTGGATGGTGTGGGGCATGATGTGTG 1858
Db 172 CCGGTCCCTCACTGTCATGGTGTCCGATTTGGGCTGGATGGTGTGGGGCATGATGTGTG 113
Qy 1859 AGGAACCTGAAGGTGCTTTAGGTCTGGTTCAGGGTCGGGCATCTTTGTTGTTGCACAT 1918
Db 112 AGGAACCTGAAGGTGAAAAAGAGTCTGGTTTCAGGGTCGGGCATCTTTGTTGTTGCACAT 53
Qy 1919 CTTTCTAAATTTTACACCTTTT 1939
Db 52 CTTTCTAAATTTTACACCTTTT 32

RESULT 34
B1739961
LOCUS
DEFINITION B1739961 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5368251 5',
mRNA sequence.
ACCESSION B1739961
VERSION B1739961.1 GI:15716974
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 964)
NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
```

Email: csapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1937 row: c column: 04
High quality sequence stop: 754.
Location/Qualifiers
1. .964
/organism="Mus musculus"
/db xref="taxon:10090"
/clone="IMAGE:5368251"
/clone_lib="NIH_MGC_94"
/tissue_types="retina"
/lab_hosts="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 283 a 199 c 247 g 234 t 1 others
ORIGIN
Query Match 23.5%; Score 476.4; DB 13; Length 964;
Best Local Similarity 81.3%; Pred. No. 7.9e-92;
Matches 645; Conservative 0; Mismatches 122; Indels 26; Gaps 7;
Qy 673 ATCATCAAGAGCTACTCTGAGGAGGACATCCACCGCTCCATTAAGTACTCCATCTCGTGT 732
Db 1 ATCATCAAGAGCTACTCTGAGGAGGACATCCACCGCTCCATTAAGTACTCCATCTCGTGT 60
Qy 733 AGCAGAGAGCGGCAACAGCGCTGACAGCGCTTCCCTGCTGATGAGGAGCAAGGG 792
Db 61 AGTACTGAACAGCGCAACAGCGCTGACAGCGCTTCCCTGCTGATGAGGAGCAAGGG 120
Qy 793 CCCGTCTACCTGCTCTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCGAGATG 852
Db 121 CCTGTTATCTCTTCAGTGTCAATGGGAGTGGGCAATTTTGTGGGTGGCGAGATG 180
Qy 853 AAGTCCCGGTGGACTACGGCACAGTGCCTGGGTCTGGTCTCAGGACAACTGGAAGGG 912
Db 181 AAGTCCCGGTGGACTACGGCACAGTGCCTGGGTCTGGTCTCAGGACAACTGGAAGGG 240
Qy 913 AAGTTGATGTCAGTGGATTTTGTGAAGATGTACCAATACCAGTCCGGCACATC 972
Db 241 AAG-TTGATGTAAGTGGATTTTGTGAAGATGTGCCCCAACCAACCAAGCTCGGCACATC 299
Qy 973 AGGTGGAGATTAACGACAAACCGGTCAAACTCCCGGGACACCCAGGAGTGCC 1032
Db 300 AGCTGGAGATTAACGACAAACCGGTCAAACTCCCGGTGATACAGAGGTGCC 359
Qy 1033 TTAGAAAAAGCAAGCAAGTCTGAAAATTAATCAAGTTCTTCAAGCACACACCTCCATC 1092
Db 360 TTAGAAAAAGCAAAACAAAGTCTGAAGATTAATCGTTCTTATAGCACACACCTCTATC 419
Qy 1093 TTCAGCAGCTTTGCTACTACAGAGAGCGCA-GAGGAGGAGGAGTGTGCGCAAGAA 1151
Db 420 TTTGACGACTTTCTCTATTATGAGAGGCGCCAGGAGGAGGAGTGTGCGTAAGAA 479
Qy 1152 CGGAGAGTGGAAACAAATGAGGGGAAACCAAGTTCTTCTACATGTTCTCACTTTTGAC 1211
Db 480 AGACAGATCGAAACAAACAAATAGAACACAGCTTTGTTGGT-----TAATGTTGAC 535
Qy 1212 TTTGAAAC--AGTTTAAACACAGTGTGCTTGGTCAGTC-----CAGTGTGT 1257
Db 536 TTTGAAACACAGATTTTAAAGCTGTATGCTTGGTGTCTCTCCGAGTCAGCTCCAGTGT 595
Qy 1258 CGTCCGTCGGGGGTGAGTGTGTCATCTTTGCTTCTTGTCTGTTGATTTTGGCCAG 1317
Db 596 CGTCCGTCGGGGGTGATTTGTCATCTTTATCTTTTGTAG-----TTCAATTTTGGCCAG 651

Qy 1318 ATGATCTGCATTTATTTGTACTTTTCTATGTATTATAATCCTGTAGACTCAATA 1377
Db 652 ATGATCTGCATTTATTTGTACTTTTCTATGTATTATAATCCTGTAGACTCAATA 711
Qy 1378 AAGAGATATTTTGTGTCAGCTTATCAATCAGACTGATCTAATGCGAAATGTAAGTAT 1437
Db 712 AAGAGTA--TGGGCGCTCAGGTTATCAGTCAGCTTATGCAAAATATAAATAT 769
Qy 1438 CCTTAAACAA 1450
Db 770 TCTTCAAGAGAA 782
RESULT 35
LOCUS BF529242 937 bp mRNA linear EST 11-DEC-2000
DEFINITION 602040117F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177805
5', mRNA sequence.
ACCESSION BF529242
VERSION BF529242.1 GI:11616605
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 937)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9485 row: a column: 06
High quality sequence stop: 634.
Location/Qualifiers
1. .937
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:4177805"
/clone_lib="NCI_CGAP_Brn67"
/tissue_types="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_hosts="DH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 242 a 183 c 214 g 297 t 1 others
ORIGIN

Query Match 23.4%; Score 475; DB 12; Length 937;
Best Local Similarity 94.9%; Pred. No. 1.6e-91;
Matches 577; Conservative 0; Mismatches 21; Indels 10; Gaps 8;
Qy 1423 GTGAAATGTAAGTATCCTTAAACAAAGCATCTATTTCGCGAGAAATGTGTTCTTAAA 1482
Db 1 GTGAAATGTAAGTATCCTTAAACAAAGCATCTATTTCGCGAGAA--TGTGTTCTTAAA 58
Qy 1483 TTGAGTCAATTTGATTTCTGTGAGCTTCATATTTCTCATCCCCCTTTATGCTTTTACGA 1542
Db 59 TTGAGTCAATTTGATTTCTGTGAGCTTCATATTTCTCATCCCCCTTTATGCTTTTACGA 118
Qy 1543 AACATAGAACCATGAGTCAATTTGTCATTTAGAGTATTCGATAAATCTCTTGA 1602
Db 119 AACATAGAACCATGAGTCA--TTTGTCAATTTAGATTTCTGTATAAATCTCTTGA 177

TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR4&t2=MR4-ST0118-
151299-023-b10&t3=1999-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 496.

FEATURES
source
1..584
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0118"
/dev_stage="Adult"
/notes="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 121 a 161 c 151 g 151 t
ORIGIN
Query Match 23.0%; Score 466.8; DB 10; Length 584;
Best Local Similarity 92.9%; Pred. No. 9.5e-90;
Matches 522; Conservative 0; Mismatches 37; Indels 3; Gaps 3;
Qy 707 GCTCATTAAGTACTCCATCTGGTGTAGCAGACGACGGCAACAGCCCTGGACACGG 766
Db 561 GCACCCCTCCATTAATCTCTCTGGTGTAGCAGACGACGGCAACAGCCCTGGACACGG 502
Qy 767 CTTTCCGCTGATGAGCAGACGAGGGCCGCTACCTCTCTTCAGCGTCAATGGAGTG 826
Db 501 CTTCCCTGGCATGAGCAGCAA-GGGCCCGCTACCTCTCTTCAGCGTCAATGGAGTG 443
Qy 827 GGCAATTTTGTGGGTGGCCGAGATGAAGTCCCGCTGGACTACGGCACCAGTGCCTGGG 886
Db 442 GGCATTTTGTGGGTGGCCGAGATGAAGTCCCGCTGGACTACGGCACCAGTGCCTGGG 383
Qy 887 TCTGGTCTCAGGACAGTGGAGGGGAATTTGATGTCCAGTGGATTTTGTAAAGGATG 946
Db 382 TCTGGTCTCAGGACAGTGGAGGGGAATTTGATGTCCAGTGGATTTTGTAAAGGATG 323
Qy 947 TACCAATAACAGCTCCGGCACATCAGCTGGAGATAACGACAAACAAACCGGTCAAA 1006
Db 322 TACCCCATTAACAGCTCCGGCACATCAGCTGGAGATAACGACAAACAAACCGGTCAAC 263
Qy 1007 ACTCCCGGGACACCCAGAGGTGCCCTTAGAAAAAGCC-AAGCAAGTGTCTGAAATATTC 1065
Db 262 ACTCCCGGGACACCCAGAGGTGCCCTTAGAAAAAGCCAGCAAGTGTCTGAAATATTC 203
Qy 1066 AGTTCTTACAGCAGACAACTCCATCTTCGACGACTTTGTCTCTACGAGAAAGCCCA- 1124
Db 202 AGTTCTTACAGCAGACAACTCCATCTTCGACGACTTTGTCTCTACGAGAAAGCCCA 143
Qy 1125 GAGGAGGAGGAGTGTGGCGCAAGGACGGCAGAGTGGAAACAAATGAGGGCGAAC 1184
Db 142 GAGGAGGAGGAGTGTGGCGCAAGGACGGCAGAGTGGAAACAAATGAGGGCGAAC 83
Qy 1185 AGTTTCTTACATGTTCTAAAGCTTTGACTTTTGAACACAGTTTAAACACAGTGTGCTTGGTC 1244
Db 82 AGTTTCTTACATGTTCTAAAGCTTTGACTTTTGAACACAGTTTAAACACAGTGTGCTTGGTC 23
Qy 1245 AGTCCAGTGTGCTCCCGTG 1266

Db 22 AGTCCAGTGTGCTGCTCGC 1
RESULT 38
AA976117
LOCUS
DEFINITION on33b10.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558459 3',
mRNA sequence.
ACCESSION AA976117
VERSION AA976117.1 GI:3151909
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 460)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgap@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.A.G.E. Consortium/LuNL at:
www.bio.lnlnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 439.

FEATURES
source
1..460
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
/notes="Organ: lung; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoma, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p7713 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 123 a 78 c 79 g 180 t
ORIGIN
Query Match 22.5%; Score 456.8; DB 9; Length 460;
Best Local Similarity 99.8%; Pred. No. 1.4e-87;
Matches 459; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1402 TATCAATCAGATGATCTAATGTGAAATGTAAGTATCTTAAAAACAAAGCATCTATTTT 1461
Db 1 TATCAATCAGATGATCTAATGTGAAATGTAAGTATCTTAAAAACAAAGCATCTATTTT 60
Qy 1462 GGCAGAAATGTGTCTTAAATTCAGTCATTTGATATTCTGTGAGACTTCATATTTCTCA 1521
Db 61 GGCAGAAATGTGTCTTAAATTCAGTCATTTGATATTCTGTGAGACTTCATATTTCTCA 120
Qy 1522 TCCCTTTATTTGCTTTTAGCAACATAAGAACCATGATCTTTTTCATTAGAGTAT 1581
Db 121 TCCCTTTATTTGCTTTTAGCAACATAAGAACCATGATCTTTTTCATTAGAGTAT 180
Qy 1582 TCTGATAAATCTCTTGAAATCTGAAATCTGAAATCTGAAATCTGAAATCTGAAATCTG 1641
Db 181 TCTGATAAATCTCTTGAAATCTGAAATCTGAAATCTGAAATCTGAAATCTGAAATCTG 240
Qy 1642 ATTTGTCAATTTTATATCTGTTATCGGTCTAAAGTGTCAATTTACCCATTTGATTTTCT 1701


```

Db 241 ATTGTGCACTTTTATATCTGTTATCGGTCTAAAGTGCCTAATTTACCCATTGATTTTCT 300
QY 1702 GCTAGACAGATACTTTTAAATTTTTCAGATTTGGCAGACACTTTTTCCTTTTGGAAA 1761
Db 301 GCTAGACAGATACTTTTAAATTTTTCAGATTTGGCAGACACTTTTTCCTTTTGGAAA 360
QY 1762 ATCTTTCTCCAGATCTGTGTGCCCCTGTAACAGCAGCACCCTGCTCCTGCTGCTGT 1821
Db 361 ATCTTTCTCCAGATCTGTGTGCCCCTGTAACAGCAGCACCCTGCTCCTGCTGCTGT 420
QY 1822 CCGATTGGGCTGATGCTGTGTGGGGATGATGTGTGGAGG 1861
Db 421 CCGATTGGGCTGATGCTGTGTGGGGATGATGTGTGGAGG 460

RESULT 39
AL580786 778 bp mRNA linear EST 16-FEB-2001
LOCUS AL580786 LTI_NFL008_Tc2 Homo sapiens cDNA clone CS0DJ014YN09 5
DEFINITION prime, mRNA sequence.
ACCESSION AL580786
VERSION AL580786.1 GI:12947147
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 778)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1. .778
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DJ014YN09"
/clone_lib="LTI_NFL008_Tc2"
/sex="male"
/tissue_type="T cells from T cell leukemia"
/notes="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 187 a 102 c 246 g 187 t 56 others
ORIGIN
Query Match 22.2%; Score 450; DB 9; Length 778;
Best Local Similarity 93.0%; Pred. No. 3.7e-86;
Matches 452; Conservative 24; Mismatches 9; Indels 1; Gaps 1;

QY 1147 AGGAAACGACAGTGCAGAAACAAATGAGCGGGAACAGTTCCTTACATGTTCTTAACGT 1206
Db 294 AGGAGCGGAGGTGGAACAAACAAATGAGCGGGAACAGTTCCTTACATGTTCTTAACGT 353
QY 1207 TTGACTTTGAAACAGTTTAAACACAGTGTGTGTGTCAGTCCAGTGTGTCGTCGCGTG 1266
Db 354 KTGRTTTTGAACACAGKTTGAAACACAGKGTGKGTGKGTGKGTGKGTGKGTGKGTGKGTG 413
QY 1267 CGGGGGTTGAGTGTGATCTTTGCCCTTCTGTCGTTGATTTTTCGCCAGATGATCTG 1326
Db 414 GGGGGGTTGAGTGTGATCTTTGCCCTTCTGTCGTTGATTTTTCGCCAGATGATCTG 473
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QY 1327 CATTATTTGTACTTTTCTATGTATTATAATCCTGTAGAGTCACTAATAAGGAGTAT 1386
Db 474 CATTATTTGTACTTTTCTATGTATTATAATCCTGTAGAGTCACTAATAAGGAGTAT 532
QY 1387 TTTTTCCTGAGCTTATCAATCAGACTGATCTAATGTCAAATGTAAGTATCCTTAAAAA 1446
Db 533 TTTTTCCTGAGCTTATCAATCAGACTGATCTAATGTCAAATGTAAGTATCCTTAAAAA 592
QY 1447 CAAAGCATCTATTTTGGCAGAAATGTGTCTTAAATTCAGTCATTGTATTTCTGTGAG 1506
Db 593 CAAAGCATCTATTTTGGCAGAAATGTGTCTTAAATTCAGTCATTGTATTTCTGTGAG 652
QY 1507 ACTTCATATTTCTCATCCCTTTATTCCTTTTGTAGCAAAACATAAGAACCATGATCATTT 1566
Db 653 ACTTCATATTTCTCATCCCTTTATTCCTTTTGTAGCAAAACATAAGAACCATGATCATTT 712
QY 1567 TGTCAATTTAGATTTCTCATAAATCTCTTGAATAATCTCTGAAATCAAAAGGTAAATGAT 1626
Db 713 TGTCAATTTAGATTTCTCATAAATCTCTTGAATAATCTCTGAAATCAAAAGGTAAATGAT 772
QY 1627 TTTTGTG 1632
Db 773 TTTTGTG 778

RESULT 40
AL524372 838 bp mRNA linear EST 13-FEB-2001
LOCUS AL524372 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC006YG03 3
DEFINITION prime, mRNA sequence.
ACCESSION AL524372
VERSION AL524372.1 GI:12787865
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 838)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1. .838
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC006YG03"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 248 a 164 c 131 g 207 t 28 others
ORIGIN
Query Match 22.0%; Score 445.2; DB 9; Length 838;
Best Local Similarity 92.4%; Pred. No. 3.9e-85;
Matches 453; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

QY 1539 AGCAACATAAGAAACCATGAGTCATTTTGTCAATTAGAGTATCTTGATAAATCTCTTG 1598
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Db 838 AGCAACATAGAAACCATGAGTCATTTTGTCAATTAGATATTTCTGTATAAATCTCTTG 779

Qy 1599 AAAATACATAAATCAAAAGGTAATGATTTTTTGTCTCAATCTGATTTTGTCAATTTAT 1658

Db 778 AAAATACATAAATCAAAAGGTAATGATTTTTTGTCTCAATCTGATTTTGTCAATTTAT 719

Qy 1659 CTGTTATCGGTCTAAAGTGCTAAATTTACCAATTTGATTTTTTCTGTAGACAGATAACTTT 1718

Db 718 CTGTTATCGGTCTAAAGTGCTAAATTTACCAATTTGATTTTTTCTGTARACAGATAACTTT 659

Qy 1719 TAAATTTTCAAAATTTGGCAGACACTTTTTTTTTTTTTTTTGGAAATCTTCTCCAGATC 1778

Db 658 TAAATTTTCAAAATTTGGCAGACACTTTTTTTTTTTTTTTTGGAAATCTTCTCCAGATC 599

Qy 1779 TGTTCGCCACTGAACAGACACCCCGTCCCTCACTGCTCTGCTGTCGGAATGGGCTGGATGG 1838

Db 598 CGTCCGCCACCGAAGACACCCCGTCCCTCACTGCTCTGCTGTCGGAATGGGCTGGATGG 539

Qy 1839 TGTTCGCCCATGATGTGGAGGAACTGGAAAGGTGCTTTAGGTCTGTTTCAAGGTTCGGC 1898

Db 538 TGTTCGCCCATGATGTGGAGGAACTGGAAAGGTGCTTTAGGTCTGTTTCAAGGTTCGGC 479

Qy 1899 ATTCTTTGTTGTTGTCATCTTTTTTAAATTTTACACCTTTTCTTAAGAATTTCTAATGCC 1958

Db 478 ATTCTTTGTTGTTGTCATCTTTTTTAAATTTTACACCTTTTCTTAAGAATTTCTAATGCC 419

Qy 1959 GTCTTAAGTTTTTATACCAATTAATGCTGAGCTTTTAAGTGTAGGATCTGTTAGTACAGACA 2018

Db 418 CCCCAAGGCTAATACCAAAATGCTGAGCTTTTAAGTGTAGGATCTGTTAGTACAGACA 359

Qy 2019 GTGTGATGGA 2028

Db 358 GTGTGATGGA 349

RESULT 41

LOCUS BG431474

DEFINITION 602495516F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4609394 5', mRNA sequence.

ACCESSION BG431474

VERSION BG431474.1 GI:13337980

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LNCMI352 row: p column: 03
High quality sequence stop: 466.
Location/Qualifiers
1. /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:4609394"
/clone_lib="NIH_MGC_75"
/lab_host="DH10B (TI phage-resistant)"
/notes="Organ: kidney; Vector: pDNR-LiB (Clontech); Site: 1: SfiI (ggcgccctcgcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:

FEATURES

source

BASE COUNT 127 a 104 c 116 g 124 t

ORIGIN

Query Match 21.9%; Score 443.4; DB 12; Length 471;
Best Local Similarity 99.4%; Pred. No. 1e-84; 1; Indels 2; Gaps 2;
Matches 466; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 909 GGGGAAGTTTGATGTCAGTGGATTTTTTGTAAAGGATGTACCCCAATAACCAAGCTCCGGCA 968

Db 2 GGGGAAGTTTGATGTCAGTGGATTTTTTGTAAAGGATGTACCCCAATAACCAAGCTCCGGCA 61

Qy 969 CATCAGCTGGAGTAATACGACAACAAACCGGTCAAACTCCCGGACACCCAGGAGGT 1028

Db 62 CATCAGCTGGAGTAATACGACAACAAACCGGTCAAACTCCCGGACACCCAGGAGGT 121

Qy 1029 GCCCTTAGAAAAAGCCCAAGTGTGAAAATTTATCAGTTTCTTACAGGAGGAGGTCTTAAAGCT 1088

Db 122 GCCCTTAGAAAAAGCCCAAGTGTGAAAATTTATCAGTTTCTTACAGGAGGAGGTCTTAAAGCT 181

Qy 1089 CATCTTCGACGACTTCTCTACTACGAGAAGCGCA - GAGGAGGAGGAGGTGGTCCGCA 1147

Db 182 CATCTTCGACGACTTCTCTACTACGAGAAGCGCAAGGAGGAGGAGGTGGTCCGCA 241

Qy 1148 GGAACGCGAGAGTCGAAACAACAATGAGGCGCAACAGTTTCTTACATGTTCTTAAAGCT 1207

Db 242 GGAACGCGAGAGTCGAAACAACAATGAGGCGCAACAGTTTCTTACATGTTCTTAAAGCT 301

Qy 1208 TGACTTTGAAAAACAGTTTAAAAACACGTTGCTGTCAGTCCAGTGTGTCCTCCGTC 1267

Db 302 TGACTTTGAAAAACAGTTTAAAAACAGTTGCTGTCAGTCCAGTGTGTCCTCCGTC 361

Qy 1268 GGGGGTT-GAGTGTGTCATCTTTGCCCTTTCTGTCGTTGATTTTGGCCAGATGGATCTG 1326

Db 362 GGGGGTTGAGTGTGTCATCTTTGCCCTTTCTGTCGTTGATTTTGGCCAGATGGATCTG 421

Qy 1327 CATTTATTTGACTTTTCTATGTTATTAATCTCTAGAGTCACATA 1375

Db 422 CATTTATTTGACTTTTCTATGTTATTAATCTCTAGAGTCACATA 470

RESULT 42

LOCUS AI536362

DEFINITION AI536362.1 GI:4450497

ACCESSION AI536362

VERSION AI536362.1

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished (1999)

COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

5'-ATTCTAGAGCCGAGCGCGGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
MGI:209275
Seq primer: -40RP from Gibco
High quality sequence stop: 463
POLYA=No.

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FEATURES
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Location/Qualifiers
1..614
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:318659"
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: p77T3D (pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA
was primed with a Not I - oligo (dT) primer [5',
TGTATCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p77T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA was kindly provided by
Dr. Minoru KO (Wayne State University)."
169 a 136 c 163 g 144 t 2 others
BASE COUNT

```

BASE COUNT	169 a	216 c	163 g	144 t	2 others
ORIGIN					
Query Match	11.8%	Score 442.4	DB 9	Length 614	
Best Local Similarity	86.3%	Pred. No. 1.6e-84			
Matches 499	Conservative	0	Mismatches 78	Indels 1	Gaps 1
Qy	667	GTGTTTCATCATCAAGAGCTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCCATC 726			
Db	2	GTGTTTCATCATCAAGAGCTATTCTTGAGGACGACATCCACCGCTCCATCAAGTACTCCATC 61			
Qy	727	TGGTCTAGCAGAGCAGCGCAACAAGCGCTGGACAGCGCTTCCGCTGCATGAGCAGC 786			
Db	62	TGGTGTAGTACTGAACACGGCAACAAGCGCTGGACGCGCTTCCGCTCCATGAGCAGC 121			
Qy	787	AAGGGGCGCGTCTACCTGCTCTTCAAGCGTCAATGGGAGTGGCGCATTTTGTGGGGTGGCC 846			
Db	122	AAGGGGCGCTGTTTATCTCTCTTCAAGTGTCAATGGGAGTGGACATTTCTGTGGGGTGGCA 181			
Qy	847	GAGATGAAGTCCCCGCTGGGATGACGGCACCAAGTGC CGGGGTCTGGTCTCAGGACAAAGTGG 906			
Db	182	GAGATGAAGTCCCCGCTGGGATGACGGCACCAAGTGC CGGGGTCTGGTCTCAGGACAAAGTGG 241			
Qy	907	AAGGGGAAGTTTGATGTCAGTGGATTTTTGTTAAGGATGTACCCAAATAACAGTCTCGG 966			
Db	242	AAGGGGAAGTTTGATGTTGAAGTGGATTTTTGTTAAGGATGTGCCCAACAACAGTCTCGG 301			
Qy	967	CACATCAGCGTGGGAGATTAACGACAAACAAACCGGTCAAACTCCCGGGACACCCAGGAG 1026			
Db	302	CACATCAGCGTGGGAGATTAACGACAAACAAACCTGTCAAACTCCCGGTATACACAGGAG 361			
Qy	1027	GTGCCCTTTAGAAAAGCCAGCAAGTGTCTGAAAATTTATCAGTTCCTTACAAGCACACAACC 1086			
Db	362	GTGCCCTTTAGAAAAGCCAAACAAGTGTCTGAAATTTATCGCTTCTTATAAGCACACAACC 421			
Qy	1087	TCCATCTTCGACGACTTTGCTCATTACGAGAAAGCGCCA-GAGGAGGAGGAGGTGTGGCG 1145			
Db	422	TCTATCTTTGACGACTTTTCTCATTTATGAGAAAGCGCCAGGAGGAAGAGGAGGTGTGGGT 481			
Qy	1146	AAGGAACGCGAGGTTCGAAAAACAAACAATGAGGGCGAAACAGTTTCTTATCATGTTCTTAACG 1205			
Db	482	AAGGAAGACAGAAATTCGAAAAACAAACAATGAGAAACAGGCGAGTTTGTGTTTGAATGGT 541			
Qy	1206	TTTGACTTTGAAAAACAGTTTAAAAACACCGTGTGCTTTGGT 1243			

Db	542	TCAGTNTGAAACACAGATTNTAAAGCTGTATGCTTGGT	579
RESULT 43			
BQ421488			
LOCUS			
DEFINITION	BQ421488	902 bp	linear mRNA
	ACENCOURT 7771914 NIH_MGC_92		Homo sapiens cDNA clone IMAGE:6014712
	5', mRNA sequence.		
ACCESSION	BQ421488		
VERSION	BQ421488.1	GI:21116803	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 902)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-t@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1AM13209 row: k column: 01 High quality sequence stop: 444. Location/Qualifiers		
FEATURES	1..902		
source	/organism="Homo sapiens"		
	/db xref="taxon:9606"		
	/clone="IMAGE:6014712"		
	/clone_lib="NIH_MGC_92"		
	/tissue_type="embryonal carcinoma, cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: testis; Vector: PCMV-SPOPT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH MGC Library."		
BASE COUNT	242 a	219 c	288 g 132 t 21 others
PERCENT			

Query Match	21.7%	Score 439.4	DB 14	Length 902
Best Local Similarity	99.8%	Pred. No. 6.8e-84		
Matches 440	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	651	TCTGAAAGCGGGGTGTTCATCATCAAGACTACTCTGAGGACGACATCCACCGCTC	710	
Db	1	TCTGAAAGCGGGGTGTGTTCATCATCAAGAGTACTCTGAGGACGACATCCACCGCTC	60	
QY	711	CATTAAGTACTCCATCTGGTGTAGCACAGACGCGCAACGCGCTTGGACAGCGCCTT	770	
Db	61	CATTAAGTACTCCATCTGGTGTAGCACAGACGCGCAACGCGCTTGGACAGCGCCTT	120	
QY	771	CGCTGCATGACGACGAAGGGCGCGTCTACTGCTCTTTCAGCGTCAATGGAGTGGGCA	830	
Db	121	CGCTGCATTTAGCAGCAAGGGCGCGTCTACTGCTCTTTCAGCGTCAATGGAGTGGGCA	180	
QY	831	TTTTTTGTGGGTGGCCGAGATGAAGTCCCGCTGGACTACGGCACAGTCCGGGGTCTG	890	
Db	181	TTTTTTGTGGGTGGCCGAGATGAAGTCCCGCTGGACTACGGCACAGTCCGGGGTCTG	240	
QY	891	GTCTCAGGACAAGTGGAAAGGGGAAGTTTGATGTCCAGTGGATTTTTTTGTTAAGGATGTACC	950	
Db	241	GTCTCAGGACAAGTGGAAAGGGGAAGTTTGATGTCCAGTGGATTTTTTTGTTAAGGATGTACC	300	
QY	951	CAATTAACGAGCTCCGGCAATCAGCGCTGGAGATTAACGACACAAACCGGTCAAACTC	1010	

```

Db 301 CAATAACGAGCTCCGGACATCAGGCTGGAGAAATACGACAAACAAACCGGTCAAAATC 360
Qy 1011 CCGGACACCCAGGAGTGCCCTTAGAAAAAGCCAAAGCAAGTGTGTAATAATATCAGTTC 1070
Db 361 CCGGACACCCAGGAGTGCCCTTAGAAAAAGCCAAAGCAAGTGTGTAATAATATCAGTTC 420
Qy 1071 CTACAAGCACACACCTCCAT 1091
Db 421 CTACAAGCACACACCTCCAT 441

RESULT 44
BM556661
LOCUS BM556661 977 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT 6540480 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737877
5', mRNA sequence.
ACCESSION BM556661
VERSION BM556661.1 GI:18798067
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 977)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.lnl.gov
Plate: L1AM12748 row: 1 column: 06
High quality sequence stop: 715.
FEATURES
source
1..977
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5737877"
/clone_lib="NIH_MGC_88"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: small intestine; Vector: pCMV-SPORT6;
Site:1: NotI; Site:2: SalI; Cloned unidirectionally;
oligo-dr primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH MGC Library."
BASE COUNT 255 a 182 c 203 g 335 t
ORIGIN
Query Match 21.4%; Score 434.4; DB 13; Length 977;
Best Local Similarity 99.6%; Pred. No. 8e-83;
Matches 446; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1581 TTCTGATAAATCTCTGAAATCTGAATCAAAAGGTTAATGATTTTGTTCATCT 1640
Db 49 TTCTATAAATCTCTGAAATCTGAATCAAAAGGTTAATGATTTTGTTCATCT 108
Qy 1641 GATTGTGTCATTTTATCTCTTATCGGTCTAAAGTGTCTAATTTACCAATTTGATTTTC 1700
Db 109 GATTGTGTCATTTTATCTCTTATCGGTCTAAGTGTCTAATTTACCAATTTGATTTTC 168
Qy 1701 TGCTAGACAGATACTTTTAATTTTCAAAATTCGCGACACTTTTTTTTTTTTGA 1760
Db 169 TGCTAGACAGATACTTTTAATTTTCAAAATTCGCGACAC-TTTTTTTTTTTTGA 227
Qy 1761 AATCTTTCTCCAGATCTGTTGCCACTGAACGCCACCGTCCCTCACTGTCCTGGT 1820
Db 228 AATCTTTCTCCAGATCTGTTGCCACTGAACGCCACCGTCCCTCACTGTCCTGGT 287

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Qy 1821 TCCGATTGGGCTGGATGGTGTGGGCATGATGTGTGAGGAACTGGAAGTGCTTTAGG 1880
Db 288 TCCGATTGGGCTGGATGGTGTGGGCATGATGTGTGAGGAACTGGAAGTGCTTTAGG 347
Qy 1881 TCTGGTTCCAGGTCGGGCATCTTTGTGTTGTTGTCACATCTTTTAAATTTTACACCTTTT 1940
Db 348 TCTGGTTCCAGGTCGGGCATCTTTGTGTTGTTGTCACATCTTTTAAATTTTACACCTTTT 407
Qy 1941 CTTAAGAATTTCTAATGCCGCTTAAAGTTTTTATACCAATTAATGCTGAGCTTTAAGTGTAG 2000
Db 408 CTTAAGAATTTCTAATGCCGCTTAAAGTTTTTATACCAATTAATGCTGAGCTTTAAGTGTAG 467
Qy 2001 GATCTGCTAGTACACAGACAGTGTGATGGA 2028
Db 468 GATCTGCTAGTACACAGACAGTGTGATGGA 495

RESULT 45
BM745209
LOCUS BM745209 435 bp mRNA linear EST 01-MAR-2002
DEFINITION K-EST0019027 S5SNU484 Homo sapiens cDNA clone S5SNU484-16-B11 5',
mRNA sequence.
ACCESSION BM745209
VERSION BM745209.1 GI:19066538
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eeoun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 16 row: B column: 11
High quality sequence stop: 435.
FEATURES
source
1..435
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S5SNU484-16-B11"
/clone_lib="S5SNU484"
/sex="M"
/tissue_type="Stomach"
/cell_type="Epithelial"
/lab_host="Top10F"
/notes="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was decapped with tabacco
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
including EcoRI site by treatment of T4 RNA ligase. The
first strand cDNA was synthesized from oligo dt-selected
mRNA by priming with dt-tailed vector. The dt-tailed
vector was adjusted to have about 60nt. The cDNA vector
was circularized with E. coli DNA ligase after digestion
of EcoRI which site is also included in vector. An RNA
strand converted to a DNA strand by Okayama-Berg method.
The obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation
method."
BASE COUNT 102 a 142 c 116 g 75 t
ORIGIN
Query Match 21.3%; Score 431; DB 14; Length 435;

```

Best Local Similarity 100.0%; Pred. No. 4.6e-82; Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 400 GCTCAGGCTCTCCAGCAGACGCCCGCTTGGCTCAACCGCAGTATCAGAGCCCTCAG 459
Db 5 GCTCAGGCTCTCCAGCAGACGCCCGCTTGGCTCAACCGCAGTATCAGAGCCCTCAG 64
QY 460 CAGCCACCCAGACCCGCTGGTGGTGGCCACGCAACAGAAACCGCGTGGGCGAGAGC 519
Db 65 CAGCCACCCAGACCCGCTGGTGGTGGCCACGCAACAGAAACCGCGGCTTGGGCGAGAGC 124
QY 520 GAGGGGCTGGCAGCGATAGCACTCTCCGGAACGCTCCAGCTAATTTGCCCCCAGC 579
Db 125 GAGGGGCTGGCAGCGATAGCACTCTCCGGAACGCTCCAGCTAATTTGCCCCCAGC 184
QY 580 GTCGAATCCCAACCCGCTCTTGAATAACTGAAGGCTGCTCACAGCTACAAACCCGAAAGAG 639
Db 185 GTCGAATCCCAACCCGCTCTTGAATAACTGAAGGCTGCTCACAGCTACAAACCCGAAAGAG 244
QY 640 TTTGAGTGAATCTGAAGAGCGGCGTGTTCATCATCAAGAGCTACTCTGAGGAGCAGC 699
Db 245 TTTGAGTGAATCTGAAGAGCGGCGTGTTCATCATCAAGAGCTACTCTGAGGAGCAGC 304
QY 700 ATCCACGCTCCATTAACTACTTCCATCTGCTGTAGCAGACGCGCAACAGCGGCTG 759
Db 305 ATCCACGCTCCATTAACTACTTCCATCTGCTGTAGCAGACGCGCAACAGCGGCTG 364
QY 760 GACAGCGCTTCCGCTCATGAGCAGCAAGCGGCGCTCTACCTGCTCTTTCAGCGTCAAT 819
Db 365 GACAGCGCTTCCGCTCATGAGCAGCAAGCGGCGCTCTACCTGCTCTTTCAGCGTCAAT 424
QY 820 GGGAGTGGGCA 830
Db 425 GGGAGTGGGCA 435
```

RESULT 46

BI224711
LOCUS 602949342F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:5093698 5',
DEFINITION mRNA sequence.

ACCESSION BI224711

VERSION BI224711.1 GI:14678155

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

plate: L1CM1861 row: c column: 11

High quality sequence stop: 584.

FEATURES

source

1. .623

/organism="Homo sapiens"

/db xref="taxon:9606"

/clone="IMAGE:5093698"

/clone lib="NIH MGC 8"

/tissue_type="Burkitt lymphoma"

/lab_host="DHI08 (phage-resistant)"

/note="Organ: lymph; Vector: pOTB7; Site:1: XhoI; Site_2:

ECORI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 179 a 141 c 155 g 148 t

ORIGIN

Query Match 21.2%; Score 430.8; DB 13; Length 623;

Best Local Similarity 89.5%; Pred. No. 4.9e-82;

Matches 544; Conservative 0; Mismatches 52; Indels 12; Gaps 7;

QY 857 CCCCCTGAGCTACGCCACAGTGC CGGGTCTG GTCTCAGGACAAAGTGGAAGGGGAAGT 916

Db 2 CCCCCTGAGCTACGCCACAGTGC CGGGTCTG GTCTCAGGACAAAGTGGAAGGGGAAGT 61

QY 917 TTGATGCTCCAGTGGATTTT TTAAGGATGTAACCAATTAACAGCTCCGCGACATCAGGC 976

Db 62 TTGATGCTCCAGTGGATTTT TTAAGGATGTAACCAATTAACAGCTCCGCGACATCAGGC 121

QY 977 TGGAGAAATAACGACAAACAAACCGGTCAAACTCCCGGGACACCCAGAGGTCCTTAG 1036

Db 122 TGGAGAAATAACGACAAACAAACCGGTCAAACTCCCGGGACACCCAGAGGTCCTTAG 181

QY 1037 AAAAAGCCAAAGCAAGTGTGAAAATTTATCAGTTCCTCAAGACACAACTCCATCTTCG 1096

Db 182 AAAAAGCCAAAGCAAGTGTGAAAATTTATCAGTTCCTCAAGACACAACTCCATCTTCG 241

QY 1097 AGCACTTTGCTACTACGAGAACGCGCA -GAGGAGAGGAGGTGGTCCGCAAGGAAGCGC 1155

Db 242 AGCACTTTGCTACTACGAGAACGCGCA -GAGGAGAGGAGGTGGTCCGCAAGGAAGCGC 301

QY 1156 AGAGTCGAAACAAACAAATGAGGGCGAACCAAGTTCTTACATACTTAACTTTGACT 1212

Db 302 AGAGTCGAAACAAACAAATGAGGGCGAACCAAGTTCTTAACTTTGACTTTGACT 361

QY 1213 TTGAAAACAG -TTTAAACACGTGTGCTTGTCTGCTAGCTCCAG -TGTTGCTCCCGTGG 1268

Db 362 TTGAAAACAGTTTAAACACAGTGTGCTTGTCTGCTAGCTCCAGATGTTGCTCCCGTGG 421

QY 1269 GGGGTTGA -GTGTTGCACTTTGCGCTT -TCCTGCTGTTGAT -TTTTGCCACATGATC 1324

Db 422 GGGGTTGACGTGTAGCATCTTTTGCCTTATCTTGTCTGTTATATATATGTTGCTCCAGATC 481

QY 1325 TGCAATTTATTTGACTTTTCTATGTTATTAATCTCTGAGAGTCACTAATAAGAGGT 1384

Db 482 TGCAATTTATTTGACTTTTCTATGTTATTAATCTCTGAGAGTCACTAATAAGAGGT 541

QY 1385 ATTTTTTTTGTGCTGCTTATCAATCAGACTGATCTAATGTGAAATGTAAATCTCTTAAA 1444

Db 542 CATACCACCGCTCAGCTTATCAATCAGACTGATCTAATGTGAAATGTAAATCTCTTAAA 601

QY 1445 AACAAAGC 1452

Db 602 CACACAAC 609

RESULT 47

R69898

LOCUS

DEFINITION

IMAGE:142344 5', mRNA sequence.

ACCESSION R69898

VERSION R69898.1 GI:843415

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman

,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,

R69898 629 bp mRNA linear EST 01-JUN-1995
Y147a01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:142344 5', mRNA sequence.

Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK

TITLE
JOURNAL
COMMENT

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

Insert Size: 957

High quality sequence stops: 381

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 957 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 381.

FEATURES

source

1. .629

/organism="Homo sapiens"

/db_xref="GDB:551383"

/db_xref="taxon:9606"

/clone="IMAGE:142344"

/clone_lib="Soares placenta Nb2HP"

/sex="Female"

/dev_stage="placenta obtained at birth (full term)"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site: Not I; Site 2: Eco RI; 1st [5'

strand cDNA was primed with a Not I - oligo(dT) primer [5'

AAC TGAAGAAATTCGCGCCGACAGAAATTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo.

144 a 101 c 139 g 238 t 7 others

BASE COUNT

ORIGIN

Query Match 21.0%; Score 426; DB 14; Length 629;

Best Local Similarity 97.8%; Pred. No. 5.3e-81;

Matches 452; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

Qy 1568 GTCATTAGAGTATTCGTGATAAAATCTCTTGAATAACTGTAATCAAAAGGTTAATGATT 1627

Db 11 GGCATTAGAGTATTCGTGATAAAATCTCTTGAATAACTGTAATCAAAAGGTTAATGATT 70

Qy 1628 TTTGTTCAATTCGTGATGTCATTTTATATCTGTTATCTGTTTAAAGTCTAATTTACC 1687

Db 71 TTTTGTTCATTCGTGATGTCATTTTATATCTGTTATCTGTTTAAAGTCTAATTTACC 130

Qy 1688 CATTTGATTTTTCTCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTT 1747

Db 131 CATTTGATTTTTCTCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTT 190

Qy 1748 TTTTTTTTTTGAATAATCTTTCTCCAGATCTGTTGCCACTGTAACAGCCACCCCTCCCT 1807

Db 191 TTTTTTTTTTGAATAATCTTTCTCCAGATCTGTTGCCACTGTAACAGCCACCCCTCCCT 250

Qy 1808 CACTGCTCTGGTGTCCGATTTGGGCTGGATGTTGTTGGGGCATGATGTTGGAGGAATCGG 1867

Db 251 CACTGCTCTGGTGTCCGATTTGGGCTGGATGTTGTTGGGGCATGATGTTGGAGGAATCGG 310

Qy 1868 AAGTGCTTTTAGGCTGTTGAGGTCGGGCAATCTTTGTTGTTGGCATCTTTTTTAAA 1927

Db 311 AAGTGCTTTTAGGCTGTTGAGGTCGGGCAATCTTTGTTGTTGGCATCTTTTTTAAA 370

Qy 1928 TTTTACACCTTTTCTTAAGAATT--CTAATGCCGCTCTTAAAGTTTTTATACCAATAATGCT 1985

Db 371 TTTTACACCTTTTCTTAAGAATTCTTAATGCCGCTCTTAAAGTTTTTATACCAATAATGCT 429

Qy 1986 GAGCTTTTAAAGTGTAGGATCTGTGTATACAGACAGTGTGATGG 2027

Db 430 GAGCTTTTAAAGTGTAGGATCTGTGTATACAGACAGTGTGATGG 471

RESULT 48

BJ044639/c

LOCUS

DEFINITION

laevis cDNA clone XL013p15 3', mRNA sequence.

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Xenopus laevis

African clawed frog.

Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 687)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tehini@genes.nig.ac.jp.

Location/Qualifiers

1. .687

/organism="Xenopus laevis"

/db_xref="taxon:8355"

/clone="XL013p15"

/clone_lib="NIBB Mochii normalized Xenopus neurula

library"

/tissue_type="whole embryo"

/dev_stage="stage 15"

/note="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs

were oligo-dT primed and directionally cloned. Staging

according to Nieuwkoop and Faber. Library is subtracted

and was constructed by N. Garrett and A.M. Zorn,

(Wellcome/CRC Institute)."

BASE COUNT 142 a 170 c 182 g 193 t

ORIGIN

Query Match 20.9%; Score 424.4; DB 13; Length 687;

Best Local Similarity 82.9%; Pred. No. 1.2e-80;

Matches 496; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

Qy 559 CAGCCTAATTCGCCCCCAGCGTCGAATCCACCCCGTCCTTTGAAAACTGAAGGCTGCT 618

Db 687 CAGTCTCAGCGTCGCCCCGGAATGAGTCTCACCTCTGCTAGAGAACTGAAGCGCC 628

Qy 619 CACAGCTACAAACCGGAAGAGTTTGAGTGGATCTGAAAACGGCGCTGTTTCATCATC 678

Db 627 CACAGCTACAAACCGGAAGAGTTTGAGTGGAACTGAAAATGGACGCTGTTTATAATA 568

Qy 679 AAGAGCTACTCTGAGGAGGACATCCCGCTCCATTAAGTACTCCATCTGTTAGTACACA 738

Db 567 AAGAGCTACTCTGAGGAGGATATCCACGTTTCCATCAATACTCAATCTGTTGACGACA 508

Qy 739 GAGCACGGCAACAAGCGCTGGACAGCGCCCTTCGCTGCATGAGCAGCAAGGGGCCCTC 798

Db 507 GAGCATGGGAATAAACGCTTGATAACGCTTTCCGCTCCATGAATGGCAAGGCCCTC 448

Qy 799 TACCTGCTCTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCGGAGATGAAGTCC 858

Db 447 TACCTTCTGTTTCAGCGTCAACGGCAGTGGACACTTTTTCGGCGTAGCGGAGATGAAGTCC 388

Qy 859 CCCGTGAGTACGGCACCAGTCCGGGTCTGGTCTCAGGACAAGTGAAGGGAAGTTT 918

Db 387 CCCGTGAGTATGGCACCCAGTCCGGGTCTGGTCTCAGGACAAGTGAAGGGAAGTTT 328

```

QY 919 GATGTCCAGTGGATTTTGTAAAGATGTACCAATAACCAAGCTCCGGCAGCATCAGGCTG 978
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 327 GAGTCAAGTGGCTCTTGTCAAGGAGCTTCCCAACACCAAGCTGAGGCACATCCGCTG 268
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 979 GAGAATAACGACAAACAAACCGGTACAAATCCCGGGACACCCAGGAGGTGCGCTTAGAA 1038
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 GAGAATAACGACAAACAAACCGGTACAAATCCCGGGACACCCAGGAGGTGCGCTTAGAA 208
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1039 AAGCCCAAGCAAGTGTGAAATATACAGTTCTCAAGCAGACCAACCTCCATCTTCGAC 1098
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 207 AAGCAAACTGTGTCTTAAATATCTTGCACATTACAAGCAGACGACCTCCATCTTTGAT 148
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1099 GACTTTGCTCACTACGAGAGCGCCA-GAGGAGGAGGAGGTGTGGCGAAGGAACGCG 1155
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 147 GACTTTCTCATACGAGAGCGCGAGGAGGAGGAGGTGTGGCGAAGGTAACG 90
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 49
AI083909/c 449 bp mRNA linear EST 10-NOV-1998
LOCUS Qf26b05.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:1751121 3'
DEFINITION similar to TR:004503 004503 SEQUENCE OF BAC F21M12 FROM ARABIDOPSIS
THALIANA CHROMOSOME 1, COMPLETE SEQUENCE. ;, mRNA sequence.
ACCESSION AI083909
VERSION AI083909.1 GI:3422332
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute / National Institute of Neurological
COMMENT Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgaops-rc@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1946 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 418.
FEATURES
source Location/Qualifiers
1. 449
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAG:1751121"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_hosts="Dh10B"
/notes="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAACTCTGAGTGGGAGCGCGCATAGTGTCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 120 a 106 c 100 g 123 t
ORIGIN
Query Match 20.9%; Score 423.4; DB 9; Length 449;
Best Local Similarity 99.3%; Pred. No. 2e-80;

```

```

Matches 446; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY 960 GCTCCGGCAGCATCAGGCTGGAGATAACGACAAACAAACCGGTACAAACTCCCGGACAC 1019
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 449 GCTCCGGCAGCATCAGGCTGGAGATAACGACAAACAAACCGGTACAAACTCCCGGACAC 390
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1020 CCAGAGGTGCGCTTAGAAAAAGCCAAAGCAAGTGTCTGAAAAATTATCAGTCTCTACAAGCA 1079
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 389 CCAGAGGTGCGCTTAGAAAAAGCCAAAGCAAGTGTCTGAAAAATTATCAGTCTCTACAAGCA 330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1080 CACAACCTCCATCTTCGACGACTTTGCTCACTACGAGAAAGCGCCA-GAGGAGGAGGAGGT 1138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 329 CACAACCTCCATCTTCGACGACTTTGCTCACTACGAGAAAGCGCCAGGAGGAGGAGGT 270
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1139 GGTGGCGAAGGAACGCGCAGAGTCGAAACAAACAAATGAGGGCGAAACAGTTTCTTACATGT 1198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 269 GGTGGCGAAGGAACGCGCAGAGTCGAAACAAACAAATGAGGGCGAAACAGTTTCTTACATGT 210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1199 TCTAACGTTTGACTTTGAAAAACAGTTTAAACACGTCGTGCTGGTCAGCTCCAGTGTGTC 1258
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 209 TCTAACGTTTGACTTTGAAAAACAGTTTAAACACGTCGTGCTGGTCAGTCCAGTGTGTC 150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1259 GTCCCGTGGCGGGGTTGAGTGTTCATCTTTGCTTTCCTTCTGTTGATTTTGGCCACA 1318
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 149 GTCCCGTGGCGGGGTTGAGTGTTCATCTTTGCTTTCCTTCTGTTGATTTTGGCCACA 90
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1319 TGGATCTGCATTTATTTGACTTTTCTATGTATTATATCTCTGTAGAAAGTCACTAATAA 1378
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89 TGGATCTGCATTTATTTGACTTTTCTATGTATTATATCTCTGTAGAAAGTCACTAATAA 30
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1379 AGAGATATTTTGTTCAGCTTATCAA 1407
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 29 AGGAGTA-TTCTTTTGTTCAGCTTATCAA 2
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 50
AI0837755/c 435 bp mRNA linear EST 04-FEB-2000
LOCUS MR4-ST0118-041099-010-A06 ST0118 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION AI0837755
VERSION AI0837755.1 GI:6892414
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 435)
JOURNAL HCGP http://www.ludwig.org.br/ORESTES.
COMMENT The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC0&t2=MR4-ST0118-
041099-010-A06&t3=1999-10-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 434.
FEATURES
source Location/Qualifiers
1. 435
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone_lib="ST0118"
/dev_stage="Adult"
/notes="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application

```

No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```
BASE COUNT      90 a  121 c  104 g  120 t
ORIGIN

Query Match      20.6%; Score 418.2; DB 10; Length 435;
Best Local Similarity 99.1%; Pred. No. 2.6e-79;
Matches 431; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 841 GTGCCGAGATGAATGCCCGTGGAGCTACGGACCAAGTCCCGGGTCTGGTCTCAGGAC 900
Db 435 GTGCCGAGATGAATGCCCGTGGAGCTACGGACCAAGTCCCGGGTCTGGTCTCAGGAC 376

Qy 901 AAGTGGAGGGAAGTTTGATGTCAGTGGATTTTGTGTTAAGGATGTACCCCAATAACGAG 960
Db 375 AAGTGGAGGGAAGTTTGATGTCAGTGGATTTTGTGTTAAGGATGTACCCCTATACGAG 316

Qy 961 CTCGGCACATCAGGCTGGAGATAAAGACAAACACCGGTCAAAAATCCCGGGACACC 1020
Db 315 CTCGAGCACATCAGGCTGGAGATAAAGACAAACACCGGTCAAAAATCCCGGGACACC 256

Qy 1021 CAGAGGTGCCCTTAGAAAAAGCAAGCAAGTGTGAAAAATTATCAGTTCTCTACAGGAC 1080
Db 255 CAGGAGTGCCTTTAGAAAAAGCCTAGCAAGTGTGAAAAATTATCAGTTCTCTACAGGAC 196

Qy 1081 ACAACCTCCATCTTCGACGACTTTCCTACACAGAGAGAGAGAGAGAGAGAGAGAGAG 1139
Db 195 ACAACCTCCATCTTCGACGACTTTCCTACACAGAGAGAGAGAGAGAGAGAGAGAGAG 136

Qy 1140 GTGGCAAGGAACGGCAGAGTCGAAACAAACAAACAGAGAGAGAGAGAGAGAGAGAGAG 1199
Db 135 GTGGCAAGGAACGGCAGAGTCGAAACAAACAAACAGAGAGAGAGAGAGAGAGAGAGAG 76

Qy 1200 CTAACGTTTGACTTTGAAAAAGAGTTTAAACACAGTGTGCTTGGTCCAGTCCAGTGTGCG 1259
Db 75 CTAACGTTTGACTTTGAAAAAGAGTTTAAACACAGTGTGCTTGGTCCAGTCCAGTGTGCG 16

Qy 1260 TCCCGTGGGGGGTT 1274
Db 15 TCCCGTGGGGGGTT 1

RESULT 51
AV725141
LOCUS      AV725141      429 bp      mRNA      linear      EST 16-OCT-2000
DEFINITION      AV725141      HTC Homo sapiens cDNA clone HTCAMH07 5', mRNA sequence.
ACCESSION      AV725141
VERSION      AV725141.1      GI:10830231
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 429)
AUTHORS      Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu
S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA HTC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. 429
/organism="Homo sapiens"
```

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/db_xref="taxon:9606"
/clone="HTCAMH07"
/clone_lib="HTC"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      125 a  59 c  57 g  188 t
ORIGIN

Query Match      20.6%; Score 418; DB 10; Length 429;
Best Local Similarity 99.8%; Pred. No. 2.8e-79;
Matches 429; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1329 TTTATTTGTAATTTTCTATGATTAATTAATCCCTGCTAGAGTCACATAAAGGAGTATTT 1308
Db 1 TTTATTTGTAATTTTCTATGATTAATTAATCCCTGCTAGAGTCACATAAAGGAGTA-TT 59

Qy 1389 TTTTTCGTGAGCTTATCAATCAGACTGATCTAATGTGAAATGTAAAGTATCTTTAAAAACA 1448
Db 60 TTTTTCGTGAGCTTATCAATCAGACTGATCTAATGTGAAATGTAAAGTATCTTTAAAAACA 119

Qy 1449 AAGCATCTATTTTGGCAGAAATTTGTGTTCTTAAATTCAGTCATTTGATATCTGTGAGAC 1508
Db 120 AAGCATCTATTTTGGCAGAAATTTGTGTTCTTAAATTCAGTCATTTGATATCTGTGAGAC 179

Qy 1509 TTCATATTTCTCATCCCTTTATTCCTTTTAGCAACATAGAAACCATGAGTCATTTTG 1568
Db 180 TTCATATTTCTCATCCCTTTATTCCTTTTAGCAACATAGAAACCATGAGTCATTTTG 239

Qy 1569 TCATTTAGAGTATTTCTGATAAAATCTCTTGAAATCTGAAATCAAAAGGTTAATGATTT 1628
Db 240 TCATTTAGAGTATTTCTGATAAAATCTCTTGAAATCTGAAATCAAAAGGTTAATGATTT 299

Qy 1629 TTTGTTCAATTCGATTTGTCATTTTATATCTGTTATCGGTCTAAAGTGCTAAATTTACCC 1688
Db 300 TTTGTTCAATTCGATTTGTCATTTTATATCTGTTATCGGTCTAAAGTGCTAAATTTACCC 359

Qy 1689 ATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTTT 1748
Db 360 ATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTTT 419

Qy 1749 TTTTTCCTTG 1758
Db 420 TTTTTCCTTG 429

RESULT 52
AV729447
LOCUS      AV729447      429 bp      mRNA      linear      EST 17-OCT-2000
DEFINITION      AV729447      HTC Homo sapiens cDNA clone HTCAMF05 5', mRNA sequence.
ACCESSION      AV729447
VERSION      AV729447.1      GI:10838868
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 429)
AUTHORS      Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu
S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA HTC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
```


JOURNAL Unpublished (2001)
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.

FEATURES
 source
 1. .687
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="XL013e02"
 /clone_lib="NIBB Mochii normalized Xenopus neurula
 library"
 /tissue_type="whole embryo"
 /dev_stage="stage 15"
 /note="vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
 were oligo-dT primed and directionally cloned. Staging
 according to Nieuwkoop and Faber. Library is substracted
 and was constructed by N. Garrett and A.M. Zorn,
 (Wellcome/CRC Institute)."

BASE COUNT 141 a 169 c 182 g 192 t 3 others
 ORIGIN

Query Match 20.3%; Score 411.6; DB 13; Length 687;
 Best Local Similarity 82.9%; Pred. No. 6.4e-78;
 Matcheb 493; Conservative 0; Mismatches 100; Indels 2; Gaps 2;

Qy 563 CTAATTTGCCCCCAGCGTGAATCCACCCCGCTTTGAAAACTGAAGCGTCTCACA 622
 Db |||||||
 Qy 686 CTCACGCTGCCCGGAAATGAGTCTCACCTGTGTAGAGAACTGAAGCGCCCA 627
 Db |||||||
 Qy 623 GCTACACCCG-AAAGATTTGAGTGAATCTGAAGCGGCGTGTTCATCATCAAG 681
 Db |||||||
 Qy 626 GCTACACCCCGAGGACTTTGACTGGAACCTGAAATGAACTGAGTGTATTAATAAG 567
 Db |||||||
 Qy 682 AGCTACTCTGAGGACGACATCCACCGCTTCCATTAAGTACTCCATCTGCTGTAGCACAGAG 741
 Db |||||||
 Qy 566 AGCTACTCTGAGGATGATATCCACCGTTCCATCAATACTCCATCTGCTGTGACACAGAG 507
 Db |||||||
 Qy 742 CACGGCAACAGCGCTGGACAGCGCTTCCGCTGCATGAGCAGAGAGGGCCGCTCTAC 801
 Db |||||||
 Qy 506 CATGGGAATAACGCTTGGATAACGCTTTCGCTCCATGAATGCAAAAGGCCGCTCTAC 447
 Db |||||||
 Qy 802 CTGCTCTTACGCTCAATGGGAGTGGCATTTTGTGGGTGGCGGAGATGAAGTCCCCC 861
 Db |||||||
 Qy 446 CTTCTGTTACGCTCAACGGCAGTGGACACTTTTGGCGCGTAGCGGAGATGAAGTCCCCC 387
 Db |||||||
 Qy 862 GTGACTACGGCACAGTGGCGGGTCTGGTCTCAGGACAAAGTGGAGGGAAGTTTGAT 921
 Db |||||||
 Qy 386 GTGACTATGGCACCAGTGGCGGTCTGGTCTCAGGACAAATGGAAGGCAAGTTTGAC 327
 Db |||||||
 Qy 922 GTCAGTGGATTTTGTAGGATGTACCCAAATACAGCTCCCGCACATCAGGCTGGAG 981
 Db |||||||
 Qy 326 GTCAAGTGGCTCTTTGTCAAGGAGCTTCCCAACACACAGCTGAGGCACATCCGCTGGAG 267
 Db |||||||
 Qy 982 AATAACGACACAAACCGGTACAAACTCCCGGACACCCAGGAGTGGCTTAGAAAA 1041
 Db |||||||
 Qy 266 AATAACGACACAAACCGGTACAAACTCCCGGACACAGGAGGTTGCCCTTAGAAAA 207
 Db |||||||
 Qy 1042 GCCAAGCAAGTGTGAAATTTATCAGTTCTTACAGCACAACCTCCATCTTCGACGAC 1101
 Db |||||||
 Qy 206 GCAAACTGGTCTTAAATCATTTGCCACTTACAGCACACGACTCCATCTTTGATGAC 147
 Db |||||||
 Qy 1102 TTGCTCACTACGAGAGCGCCA-GAGGAGGAGAGGTGGTGGCCAAAGGAACGCG 1155
 Db |||||||
 Qy 146 TTTTCTCATACGAGAGCGCAGGAGAGAGAGGTGGTGGCCAAAGGTAACGC 92
 Db |||||||

RESULT 55
 BM745243
 LOCUS

EST 01-MAR-2002

DEFINITION K-EST0019074 SSSNU484 Homo sapiens cDNA clone SSSNU484-16-F12 5',
 mRNA sequence.
 ACCESSION BM745243
 VERSION BM745243.1 GI:19066572
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 432)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 CONTACT: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongseung@mail.kribb.re.kr
 Plate: 16 row; F column: 12
 High quality sequence stop: 432.

FEATURES
 source
 1. .432
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="SSSNU484-16-F12"
 /clone_lib="SSSNU484"
 /sex="M"
 /tissue_type="Stomach"
 /cell_type="Epithelial"
 /cell_line="SNU-484"
 /lab_host="top10r"
 /note="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI;
 Site 2: NotI; The poly (A) + RNA was decapped with tabacco
 acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
 including EcoRI site by treatment of T4 RNA ligase. The
 first strand cDNA was synthesized from oligo dT-selected
 mRNA by priming with dr-tailed vector. The dr-tailed
 vector was adjusted to have about 60nt. The cDNA vector
 was circularized with E. coli DNA ligase after digestion
 of EcoRI which site is also included in vector. An RNA
 strand converted to a DNA strand by Okayama-Berg method.
 The obtained cDNA vectors were used for transformation of
 competent cells E. coli top10r' by electroporation
 method."

BASE COUNT 99 a 142 c 116 g 75 t
 ORIGIN

Query Match 20.3%; Score 411; DB 14; Length 432;
 Best Local Similarity 100.0%; Pred. No. 9e-78;
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 400 GCTCAGGCTCTCCAGCACAGCCCCAGCTTTGGCTCAACCGCAGTATCAGAGCCCTCAG 459
 Db |||||||
 Qy 5 GCTCAGGCTCTCCAGCACAGCCCCAGCTTTGGCTCAACCGCAGTATCAGAGCCCTCAG 64
 Db |||||||
 Qy 460 CAGCCACCCAGACCCCGCTGGGTGGCCCCACGCAACAGAACCGCGCTTTGGGACAGC 519
 Db |||||||
 Qy 65 CAGCCACCCAGACCCCGCTGGGTGGCCCCACGCAACAGAACCGCGCTTTGGGACAGC 124
 Db |||||||
 Qy 520 GGAGGGGCTGGCAGCGATAGCAACTCTCTGGAAACGTCAGCCTTAATCTGCCCCCAGC 579
 Db |||||||
 Qy 125 GGAGGGGCTGGCAGCGATAGCAACTCTCTGGAAACGTCAGCCTTAATCTGCCCCCAGC 184
 Db |||||||
 Qy 580 GTCGAATCCACCCCGCTCTTGAATAACTCAAGGCTGCTCACAGCTACAAACCCGAAAGAG 639
 Db |||||||
 Qy 185 GTCGAATCCACCCCGCTCTTGAATAACTCAAGGCTGCTCACAGCTACAAACCCGAAAGAG 244
 Db |||||||
 Qy 640 TTTGAGTGGGAATCTGAAACCGCGCGTGTTCATCATCAAGAGCTACTCTGAGGACGAC 699
 Db |||||||

```

Db 245 TTTAGTGGATCTGAAGCGGGCGTGTTCATCATCAAGAGCTACTCTGAGGAGC 304
QY 700 ATCCACCGTCCATTAAGTACTCCATCTGGTGTAGCAGACGCGCAACAGCGCTG 759
Db 305 ATCCACCGTCCATTAAGTACTCCATCTGGTGTAGCAGACGCGCAACAGCGCTG 364
QY 760 GACAGCGCTTCGGCTGCATGACGACGAGGCGCGCTTACCTGCTCTTC 810
Db 365 GACAGCGCTTCGGCTGCATGACGACGAGGCGCGCTTACCTGCTCTTC 415

RESULT 56
LOCUS B0737180 916 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT 8148583 NICHD XGC Emb4 Xenopus laevis cDNA clone
IMAGE:5542099 5', mRNA sequence.
ACCESSION B0737180
VERSION B0737180.1 GI:21876077
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 916)
REFERENCE NC1-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NC1-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Plate: LLAM12240 row: n column: 20
High quality sequence stop: 615.

FEATURES
source
1..916
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:5542099"
/clone_lib="NICHD XGC Emb4"
/dev_stage="embryo, stage 31-32"
/lab_host="DH10B (phage-resistant)"
/note="Organ: whole embryo; Vector: pCMV-SPORT6; Site: 1:
NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo
dt. Average insert size 2.1 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC
) library."
BASE COUNT 255 a 250 c 226 g 183 t 2 others
ORIGIN
Query Match 20.1%; Score 407.6; DB 14; Length 916;
Best Local Similarity 75.3%; Pred. No. 4.5e-77;
Matches 561; Conservative 0; Mismatches 175; Indels 9; Gaps 4;

QY 400 GCTCAGCCTTCCAGCAGACGCGCCAGCTTTGGCTCAACCGCAGTATCAGACGCTCAG 459
Db 44 GCTCAGCCTTCCAGCAGTGTCTCAGCCTCCATATCAAAATCCAGCGCCCTCAGCAGCCA 103
QY 460 CAGCCACCCAGACCGCTGGTGGCCCGCAGCAGAAACGGCGTTGGCGCAGC 519
Db 104 CAGTCCCTCAGAAATCGTTGGTGGCCCGCAGGAATAGGAACGCTTACGGTCAGG 163
QY 520 GGAGGGGCTGGCAGCGATAGCACTCTCTCTGGAAACGCTCCAGCTATTCTGCCCGCCAGC 579
Db 164 GGAGGCCAACACGGG-----ACCCCTTTGGGAGGAGTCCAGGCTCATGCTGCCCTTGA 217
QY 580 GTCGAATCCACCCCGCTCTTTGAAAACTGAAGGCTGCTCACAGCTACAAACCCGAAAGAG 639

```

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Db 218 AACGAATCTCACCTTGTCTAGAGAACTGAAGCGCGTCCACAGCTACAAACCCAGGAC 277
QY 640 TTTAGTGGAAATCTGAAAAGCGGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGAGC 699
Db 278 TTTAGTGGAACTGAAAATGAAGCGTGTGTTTATTAATAAAGAGCTATTCTGAGGATGAT 337
QY 700 ATCCACCGCTCCATTAAGTACTCCATCTGGTGTAGCAGACGCGCAACAGCGCTG 759
Db 338 ATCCACCGTTCATCAATACTCCATTTGGTGCAGACAGAGCATGGGAATAAACGCTG 397
QY 760 GACAGCGCTTCGGCTGCATGACGACGAGGCGCGTCTTACCTGCTCTTCACGCTCAAT 819
Db 398 GATAGCGCTATCCGCTCCATGAATGAAGAGCGCGGTCTACCTCTGTTACGCTCAAC 457
QY 820 GGAGTGGGCACTTTTGTGGGGTGGCCGAGAGTGAAGTCCCCCGTGGAGTACTACGCCACAGT 879
Db 458 GGCAGTGGACACTTCTGCGCGGTAGCCGAGATGAAGTCCCGGTGGACTATGSCACAGT 517
QY 880 GCGGGGCTCGTCTCAGGACAAAGTGAAGGGAAGTTTGATGTCCAGTGGATTTTGT 939
Db 518 GCAGGTGTCTGGTCAACAGCAAAATGAAGGGCAAGTTTGACGTCAAGTGGCTCTTTGTC 577
QY 940 AAGGATGATCCCAATAAACAGCTCCGCGCACAT-CAGGCTGGAGAAATAAGCAGCAACAAACC 998
Db 578 AAGAGCTTCCCAACAAACAGCTGAGGCAATNCCGCTGGAGAACAAACGACAAACACC 637
QY 999 GGTCAAAAACCTCCG-GGACACCCAGGAGTGCCCTTAGAAAAAGGCAAGTAGTGTGA 1057
Db 638 GGTCAAAAACCTCCGAGAACACGACGAGGTGCCCTTAGAAAAAGGCAAGTAGTGTGA 697
QY 1058 AAATATCATAGTCTCTACAGCACAAACCT-CAATCTTCGACGACTTTGCTCTACTAGGAG 1116
Db 698 AAATCATTCGCACTTACAAGCACACGACCTCCCATCTTTGATGACTTTTCTCATTACGAG 757
QY 1117 AAGCGCAGAGGAGGAGGTGGT 1141
Db 758 AAGCGCAGGAANAAAGAGGT 782

RESULT 57
LOCUS AV747364 548 bp mRNA linear EST 19-OCT-2000
DEFINITION AV747364 NPC Homo sapiens cDNA clone NPCBK10 5', mRNA sequence.
ACCESSION AV747364
VERSION AV747364.1 GI:10905212
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 548)
REFERENCE Qian, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N.,
AUTHORS Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu
, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Ye, M., Zhang, Q.
, Han, Z., Chen, Z., Hu, R. and Chen, J.
Homo sapiens NPC library cDNA clones
Unpublished (2000)
Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045 (ex. 663332)
Fax: 86-21-64743206
Email: mbshi@ms.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.

FEATURES
Location/Qualifiers
1..548
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NPCBK10"

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/clone="CSODI040YK06"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="pituitary"
/dev_stage="Adult"
/lab_host="SOLR"
/notes="vector: pbluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 149 a 118 c 127 g 143 t 11 others
ORIGIN

Query Match 20.0%; Score 406.6; DB 10; Length 548;
Best Local Similarity 91.0%; Pred. No. 7.7e-77;
Matches 483; Conservative 0; Mismatches 42; Indels 6; Gaps 5;

QY 915 GTTTGATGTCACGAGGATTTTGTAGAGATGTACCCAAATACAGCTCCGGCACATCAG 974
DB 1 GGTGTGATGGGAGCCGAGCTTACAGGACGACACCTCAGCAAGCCCGCGGATGAACAG 60

QY 975 GCTGGAGATTAACGACAAACAAACCGGTCAAAATCCCGGACACCCAGGAGGTGCCCTT 1034
DB 61 CCTGGAGATTAACGACAAACAAACCGGTCAAAATCCCGGACACCCAGGAGGTGCCCTT 120

QY 1035 AGAAAAGCCCAAGCAGCTGCAAAATATCAGTTCTTACAGCAGACACAACTCCATCTT 1094
DB 121 AGAAAAGCCCAAGCAGCTGCAAAATATCAGTTCTTACAGCAGACACAACTCCATCTT 180

QY 1095 CGAGCACTTTGCTCACTACGAGAGCGCCA--GAGGAGGAGGAGGTGGTGGCGAAGGAACG 1153
DB 181 CGAGCACTTTGCTCACTACGAGAGCGCCAGGAGGAGGAGGTGGTGGCGAAGGAACG 240

QY 1154 GCAGAGTGAACAAACAAATGAGGGCGAACCCAGTTTCTTACATGTTCTTAACGTTTGACTT 1213
DB 241 GNAAGTCNAAACAAACAAATGAGGGCGAACCCAGTTTCTTACATGTTCTTAACGTTTGACTT 300

QY 1214 TGAACACAGTTTAAACACAGTGTGCTGGTCACTCCAGTGTGCTCCCGTGGGGGGT 1273
DB 301 TGAACACAGTTTAAACACAGTGTGCTGGTCACTCCAGTGTGCTCCCGTGGGGGGT 359

QY 1274 TGAGTGTGTCATCTTGGCTTTCTGCTGTTGATTTTGGCCAGATGATCTGCATTTAT 1333
DB 360 TGAGTGTGTCATCTTGGCTTTCTGCTGTTGATTTTGGCCAGATGATCTGCATTTAT 418

QY 1334 TTGTACTTTTCTAGTATTATAATCTGTTAGAGTCACTAATAAGGAGTATTTTTTTT 1393
DB 419 TTGTACTTTTCTAGTATTATAATCTGTTAGAGTCACTAATAAGGAGTATTTTTTTT 477

QY 1394 TGTGAGCTTATCAATCAGACTGATCTATGTGAATGTGAATGTAATCTCTTAAA 1444
DB 478 --GCAGCTTATCAATCAGACTGATCTATGTGAATGTGAATGTAATCTCTTAAA 526

RESULT 58
AL550164
LOCUS AL550164 LTI_NFL006_PL2 1053 bp mRNA linear EST 16-FEB-2001
DEFINITION prime, mRNA sequence.
ACCESSION AL550164
VERSION AL550164.1 GI:12898688
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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source
1. .1053
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/db_xref=taxon:9606"
/clone="CSODI040YK06"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="pituitary"
/dev_stage="Adult"
/lab_host="SOLR"
/notes="vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 198 a 349 c 314 g 191 t 1 others
ORIGIN

Query Match 20.0%; Score 405.8; DB 9; Length 1053;
Best Local Similarity 98.3%; Pred. No. 1.1e-76;
Matches 410; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAAAAGGACAGGATTAATAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 60
DB 366 CAAAAGGACAGGATTAATAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 425

QY 61 ACAATGACTTTAGCCCTTACCTTACTGGACAGTCAAAATCAGAGTAACAGTTTACCCCTCAA 120
DB 426 ACAATGACTTTAGCCCTTACCTTACTGGACAGTCAAAATCAGAGTAACAGTTTACCCCTCAA 485

QY 121 TGACGACCCCTTACCTTCTCAGCTTATTACCGCGCTCCATTGGATTTCTTCTTCTCTCA 180
DB 486 TGACGACCCCTTACCTTCTCAGCTTATTACCGCGCTCCATTGGATTTCTTCTTCTCTCA 545

QY 181 ATGAGGCTCGTGTCTACTGCGAGGACCCCTCGATTCATACCTCACACCTACCGGAC 240
DB 546 ATGAGGCTCGTGTCTACTGCGAGGACCCCTCGATTCATACCTCACACCTACCGGAC 605

QY 241 AGCTCAGTAACGAGACATCATTTTATGACAGTGTCTGTTTGGGCGAGCTCGGGGGCC 300
DB 606 AGCTCAGTAACGAGACATCATTTTATGACAGTGTCTGTTTGGGCGAGCTCGGGGGCC 665

QY 301 TGGGGAACAACATCTATCAGACAGGTTCAATTTTTTCCCTGAAAAACCTCGGTTCTCAG 360
DB 666 TGGGGAACAACATCTATCAGACAGGTTCAATTTTTTCCCTGAAAAACCTCGGTTCTCAG 725

QY 361 CATGGGGACAAAGTGGCTCTCAGGTCAGACCCAGAGCTCAGCTCTCCACGCA 417
DB 726 CATGGGGACAAAGTGGCTCTCAGGTCAGACCCAGAGCTCAGCTCTCCACGCA 782

RESULT 59
AL514504
LOCUS AL514504 LTI_NFL006_PL2 977 bp mRNA linear EST 13-FEB-2001
DEFINITION prime, mRNA sequence.
ACCESSION AL514504
VERSION AL514504.1 GI:12777998
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1. .977
/organism="Homo sapiens"
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Matches 537; Conservative 0; Mismatches 112; Indels 18; Gaps 5;

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Qy 787 AAGGGGCGGCTTACCTGCTCTTCAAGCTCAATGGAGTGGGCAATTTTGTGGGTGGCC 846
Db 5 AGGGGGCGGTTTATCTCTCTCAAGTGTCAATGGAGTGGGCAATTTTGTGGGTGGCA 64
Qy 847 GAGATGAATCCCCCGTGGACTACGGCACAGTCCCGGGTCTGCTCTCAGGACAAGTGG 906
Db 65 GAGATAAAGTCCCTGTGGATTACGGCACAGCGTGGGGTCTGCTCTCAGGACAAGTGG 124
Qy 907 AAGGGGAAGTTTGATGTCCAGTGGATTTTGTGAAGGATGTACCAATTAACAGCTCCG 966
Db 125 AAGGGGAAGTTTGATGTGAAGTGGATTTTGTGAAGGATGTCCCAACACAGCTGGG 184
Qy 967 CACATCAGGCTGGAGAATAACGACAACAAACCGGTCAAAACTCCCGGACACCCAGAG 1026
Db 185 CACATCAGACTGGAGAATAACGACAACAAACCTGTCAAAACTCCCGGTATACAGAG 244
Qy 1027 GTGCCCTTAGAAAAAGCCAAAGTGTCTGAATTTATTCAGTTCTTACAGCACACAC 1086
Db 245 GTGCCCTTAGAAAAAGCCAAAGTGTCTGAAGATTATCGCTTCTTATAAGCACACAC 304
Qy 1087 TCCATCTTCGACGACTTTGCTCACTACGAGAGCGCCA-GAGGAGGAGGAGTGTGGC 1145
Db 305 TCTATCTTTGACGACTTTTCTATTATGAGAGCGCCAGGAGGAGGAGTGTGGCT 364
Qy 1146 AAGAAAGGAGAGTCGAAACAAACAAATAGAGGGGAAACAGTCTTTTACATGTCTAACG 1205
Db 365 AAGAAAGACAGAAATCGAAACAAACAAATAGAAACAGCAAGTGTGTTTGTGTTAATGGT 424
Qy 1206 TTTGACTTTGAAACAGTTTAAACACAGTGTCTTGTGTCACT-----CCAGTG 1254
Db 425 TGACTTTTGAACACAGAGTTTAAAGCTGTATGCTTGTGTCTCCGAGTCAGTCCAG 484
Qy 1255 TGTGCTCCGCGCGGGGTTGAGTGTGCACTTTGCTTGTGCTTGTGCTGATTTTGGC 1314
Db 485 TGTGCTCTCTGCGGGGTGATTTGTCATCTTTATCTTTGTAG----TTCAITTTTGC 540
Qy 1315 CAGATGATCTGCATTTTATTTGTACTTTTCTATGATTAATAATCCTGTAGAAGTCACTA 1374
Db 541 CAGATGATCTGCATCTTATTGTA-TTTTCTATGATTAATAATTTAGAACTCACTA 599
Qy 1375 ATAAGGAGTATTTTGTGTCAGCTTATCAATCAGACTGATCTAATGTAAGTGAAG 1434
Db 600 ATAAGGAGTATTTTGTGTCAGCTTATCAGTCACTGATGACCTAATGCAAAATATAA 658
Qy 1435 TATCCTT 1441
Db 659 TATCTT 665
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RESULT 61
AW138532/c
LOCUS
DEFINITION
  UI-H-BII-abx-d-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
  IMAGE:2713371 3', mRNA sequence.
ACCESSION
  AW138532
VERSION
  AW138532.1 GI:6142850
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 441)
AUTHORS
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgaps-remail.nih.gov
  The sequence contained an oligo-dr track that was present in the
  oligonucleotide that was used to prime the synthesis of first
  strand cDNA and therefore this may represent a bonafide poly A
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tail. cDNA Library Preparation: M.B. Soares Lab Clone Distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.

FEATURES

source

1. 441
/location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2713371"
/lab_host="NCI CGAP Sub3"
/notes="vector: pr773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; The
NCI CGAP Sub3 library is a subtracted library derived from
the NCI CGAP Sub1 library, which is a subtracted library
derived from B1. B1 constitutes a mixture of 21
normalized or subtracted NCI CGAP libraries: NCI_CGAP_Co4
, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10,
NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2,
NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1, NCI_CGAP_Le12,
NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
NCI_CGAP_Lu19, NCI_CGAP_Gc4, NCI_CGAP_Gc6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683,
3798-3803 (IMAGE CloneIDs 132376-1323911, 1456008-1456775
, 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3342
, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831,
1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1
LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991,
1520904-1522439); NCI_CGAP_Gc4 pool 1 LLAM 3164-3167,
3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,
1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1
LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs
98508-986759, 1101192-1101959, 1217928-1220615);
NCI_CGAP_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE
CloneIDs 1057416-1061255, 1144584-1145351). Subtraction
was performed as previously described (Bonald, Lemmon &
Soares (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery. Genome Research
6, 791-806.
TAG_LTB=NCI_CGAP_Lu5
TAG_TISSUE=Lung
TAG_SEQ=CAAC"

BASE COUNT 117 a 100 c 93 g 131 t
ORIGIN

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Query Match 19.6%; Score 397.6; DB 10; Length 441;
Best Local Similarity 98.8%; Pred.No. 6.7e-75;
Matches 411; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 979 GAGAATAACGACACAAACCGGTCAAAACTCCCGGACACCCAGGAGTCCCTTAGAA 1038
Db 441 GAGAATAACGACACAAACCGGTCAAAACTCCCGGACACCCAGGAGTCCCTTAGAA 382

Qy 1039 AAGCCCAAGCAAGTCTGAAATTTATCAGTTCTTACAGCACACAACTTCATCTTCAC 1098
Db 381 AAGCCCAAGCAAGTCTGAAATTTATCAGTTCTTACAGCACACAACTTCATCTTCAC 322

Qy 1099 GACTTTCTCTACTACGAGAGCGGCA-GAGGAGGAGGAGTGGTGGCCAGGAGGAGCAG 1157
Db 321 GACTTTCTCTACTACGAGAGCGGCA-GAGGAGGAGGAGTGGTGGCCAGGAGGAGCAG 262

Qy 1158 AGTCGAACAAACAAATGAGGCGCAACCACTTTCTTACATGTTCTTAACGTTTGA 1217
Db 261 CGTCGAACAAACCAATGAGGCGCAACCACTTTCTTACATGTTCTTAACGTTTGA 202

Qy 1218 AACAGTTTAAACACAGTGTGCTGGTCAGCTCCAGTGTGTCGTCCTCGGGGGTTGAG 1277
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Db 201 AACAGTTTAAACACAGTGTGCTTGGTCAGCTCCAGTGTGTCGTCCTGGGGGTTGAG 142
QY 1278 TGTGTGATCTTTGCTTGTGCTTGTGATTTTGGCCAGATCGATCTGCATTTATTTGT 1337
Db 141 TGTGTGATCTTTGCTTGTGCTTGTGATTTTGGCCAGATCGATCTGCATTTATTTGT 82
QY 1338 ACTTTTCTATGATTATATATCTGTAGAGTCACTAATAAGAGGATTTATTTT 1393
Db 81 ACTTTTCTATGATTATATATCTGTAGAGTCACTAATAAGAGGATTTATTTT 26

RESULT 62
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LOCUS AL526609 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC020Y104 5
DEFINITION prime, mRNA sequence.
ACCESSION AL526609
VERSION AL526609.1 GI:12790102
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 826)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..826
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC020Y104"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 168 a 270 c 239 g 147 t 2 others
ORIGIN
Query Match 19.5%; Score 396.4; DB 9; Length 826;
Best Local Similarity 98.3%; Pred. No. 1.1e-74;
Matches 411; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 CAAGAAGACAGATATAAAGTCAAAATGGTTGTTACATCAGAGATACAGTTTCATG 60
Db 270 CAAGAAGACAGATATAAAGTCAAAATGGTTGTTACATCAGAGATACAGTTTCATG 329
QY 61 ACAATGACTTTGAGCCCTACTCTTACTCGACATCAATCAGATTAACAGTTTACCCTCAA 120
Db 330 ACAATGACTTTGAGCCCTACTCTTACTCGACATCAATCAGATTAACAGTTTACCCTCAA 389
QY 121 TGAGCGACCCCTACTCTGTCAGCTATTACCGCGCTCCATTGGATTTCTTACTCCCTCA 180
Db 390 TGAGCGACCCCTACTCTGTCAGCTATTACCGCGCTCCATTGGATTTCTTACTCCCTCA 449
QY 181 ATGAGGCTCGGTGCTTACTGCGAGGACCCCTCGATTCATACCTCACCACCTACGGAC 240
Db 450 ATGAGGCTCGGTGCTTACTGCGAGGACCCCTCGATTCATACCTCACCACCTACGGAC 509

QY 241 AGCTCAGTAAACGAGACCATCATTTTATCAAGATCTGTTTTTGGGAGCCTTGGGGGCC 300
Db 510 AGCTCAGTAAACGAGACCATCATTTTATGACGATCTGTTTTTGGGAGCCTTGGGGGCC 569
QY 301 TGGGGAAACACAT-CTATCAGCACAGGTTCAATTTTCCCTGAAACCTCGGTTCTCA 359
Db 570 TGGGGAAACACATCTATCAGCACAGGTTCAATTTTCCCTGAAACCTCGGTTCTCA 629
QY 360 GCATGGGGGACAAAGTGGGTCTCAAGGTCAAGACACAGAGCTCAGCCTCTCCAGCA 417
Db 630 GCATGGGGGACAAAGTGGGTCTCAAGGTCAAGACACAGAGCTCCGGTATGGGAGCA 687

RESULT 63
AL656188 702 bp mRNA linear EST 13-DEC-2001
LOCUS AL656188 XGC-neurula Silurana tropicalis cDNA clone TNeu035i07 5',
DEFINITION mRNA sequence.
ACCESSION AL656188
VERSION AL656188
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 702)
AUTHORS Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
TITLE Sanger Xenopus tropicalis EST project 2001 (10_2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Huckle E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu035i07.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.

FEATURES
source
1..702
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu035i07"
/clone_lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dt primed from sug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT 162 a 254 c 185 g 100 t 1 others
ORIGIN
Query Match 19.3%; Score 390.6; DB 9; Length 702;
Best Local Similarity 80.9%; Pred. No. 2e-73;
Matches 469; Conservative 0; Mismatches 105; Indels 6; Gaps 1;

QY 436 CAACCGCAGTATCAGAGCCCTCAGCAGCCACCCAGACCGCTGGTTGCCCCACGCAAC 495
Db 129 CCACCGCCCTCAGCAGCAGCCACCGCCCTCAGAACCGCTGGGTGGGCCCCACGCAAC 188
QY 496 AGAAGCGCGCTTTGGGACAGCGGGGCTGGGCGGATAGCACTCTCTGGAAAC 555
Db 189 AGAAGCGCTCTTACGCGCAGCGGGGCGGAGCCCGGAGC-----GGAACCTCTGGGGCGG 242
QY 556 GTCAGCCTAAATCTGCCCCCAGCGTCGAATCCACCCCTCTTGAAGAACTGAAGSCT 615
Db 243 GCTCAGTCTCACTCCGCCCCCTGGGAACGAGTCCACCCCTGCTGGAGAACTGAAGSCT 302
QY 616 GCTCAGCTACCAACCGGAAGAGTTTGAGTGAATCTGAAAGCGGGCGGTGTTTCATC 675

Db 303 GCCCAGCTACACCCCAAGACTTTGACTGGAACTGAAACCGGGCGGTGTCATA 362

Qy 676 ATCAAGAGTACTCTGAGGAGGACATCCACCGCTCCATTAAGTACTCCATCTGGTGTAGC 735

Db 363 ATAAAGAGTACTCGAGGAGGACATCCACCGCTCCATCAAGTACTCCATCTGGTGCAGC 422

Qy 736 ACAGAGCAGGCAACAAAGCGCTTGACAGCGCTTCCCTGCTGATGAGCAGCAAGGGGCC 795

Db 423 ACAGAGCAGGCAACAAAGCGCTTGATAGCGCTTCCGCTCCATGAACGCAAGGGCCCC 482

Qy 796 GTCTACCTGCTCTTCAAGGCTCAATGGGAGTGGGCAATTTTGTGGGTGGCCGAGATGAAG 855

Db 483 GTCTACCTTCTGTTCAAGGCTCAACGGCAGCGGACACTTCTGCGCGTGGCCGAGATGAAG 542

Qy 856 TCCCGCGTGGACTACGGCACCAGTCCCGGGGTCTGGTCTCAGGACAACTGGAAGGGGAAG 915

Db 543 TCCCGCGTGGACTACGGCACCAGTCCCGGGGTCTGGTCTCAGGACAACTGGAAGGGGAAG 602

Qy 916 TTTGATGTCAGTGGATTTTGTAAAGGATGTACCCAAATACCAAGCTCCGCGCACATCAGG 975

Db 603 TTCGACGTCAGTGGCTCTTCTGTCNCAAGACGTTCCCAACAAACCAGCTGAGGCACATCCG 662

Qy 976 CTGAGATATACGACCAACAAACCGGTCAACAACTCCCGG 1015

Db 663 CTGAGATATACGACCAACAAACCGGTCAACAACTCGCGG 702

RESULT 64

AL524373

LOCUS AL524373 LTI_NFL003_NBC3 820 bp mRNA linear EST 13-FEB-2001

DEFINITION AL524373 prime, mRNA sequence.

ACCESSION AL524373

VERSION AL524373.1 GI:12787866

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 820)

AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

location/Qualifiers

1..820

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DC006VG03"

/clone_lib="LTI_NFL003_NBC3"

/sex="male"

/tissue_type="neuroblastoma cells"

/lab_host="DH10B"

/notes="Organ: brain; Vector: pcMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 152 a 242 c 242 g 153 t 31 others

ORIGIN

Query Match 19.3%; Score 390.6; DB 9; Length 820;

Best Local Similarity 92.3%; Pred. No. 26-73;

Matches 385; Conservative 21; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CAAAGGCAAGATAATAAAGTACAAAATGGTTCGTTACATCAGAAGGATACAGTTTCATG 60

Db 275 CAAAGGCAAGATAATAAAGTACAAAATGGTTCGTTACATCAGAAGGATACAGTTTCATG 334

Qy 61 ACATGACTTTGAGCCCTACCTTACTGACAGTCAATACAGTAAACAGTTACCCCTCAA 120

Db 335 ACATGATGTTTGGCAGTCACTTWTGGCAGTAAATYAGAGTTACAGTTACCTCTCAA 394

Qy 121 TGAGCGACCCCTACTCTGTCAGCTATTACCGCGCTGTCATTTGGATTTCTTACTCCCTCA 180

Db 395 TGAGCGACCCCTACTCTGTCAGCTATTACCGCGCTGTCATTTGGATTTCTTACTCCCTCA 454

Qy 181 ATGAGGCTCCGTTGCTACTGTCAGGGACCCCTCCGATTTCATACCTCACACCTACAGGAC 240

Db 455 ATGAGGCTCCGTTGCTACTGTCAGGGACCCCTCCGATTTCATACCTCACACCTACAGGAC 514

Qy 241 AGCTCAGTAACGAGACCATCATTTTATGACAGTGTCTTTTGGGAGCGCTGGGGGCC 300

Db 515 AGCTCAGTTACGAGACCATCATTTTATGACAGTGTCTTTTGGGAGCGCTGGGGGCC 574

Qy 301 TGGGGAACAACATCTATCAGCACAGGTTCAATTTTCCCTGAAACCCCTGCGTTCTCAG 360

Db 575 TGGGGAACAACATCTATCAGCACAGGTTCAATTTTCCCTGAAACCCCTGCGTTCTCAG 634

Qy 361 CATGGGGACAAGTGGGTCTCAAGGTCAGCAGACCCAGAGCTCAGCTCTCCAGCA 417

Db 635 CATGGGGACAAGTGGGTCTCAAGGTCAGCAGACCCAGAGCTCAGCTCTCCAGCA 691

RESULT 65

AL558224

LOCUS AL558224 LTI_NFL008_TC2 773 bp mRNA linear EST 16-FEB-2001

DEFINITION AL558224 prime, mRNA sequence.

ACCESSION AL558224

VERSION AL558224.1 GI:12902542

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 773)

AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

location/Qualifiers

1..773

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DJ001YF07"

/clone_lib="LTI_NFL008_TC2"

/sex="male"

/tissue_type="T cells from T cell leukemia"

/notes="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 154 a 260 c 219 g 139 t 1 others

ORIGIN

Query Match 19.0%; Score 385.4; DB 9; Length 773;

Best Local Similarity 98.1%; Pred. No. 2.6e-72;

Matches 411; Conservative 0; Mismatches 6; Indels 2; Gaps 2;


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QY 1 CAAAGGACAGGATAATAAAGTACAAATGGTTCGTTACATCAGAAAGGATACAGTTTCATG 60
|
|
Db 277 CAAAGGACAGGATAATAAAGTACAAATGGTTCGTTACATCAGAAAGGATACAGTTTCATG 336
|
|
QY 61 ACAATGACTTTGAGCCCTACCTTACTGAGGAGTCAATCAGAGTAAACAGTCCCTCAA 120
|
|
Db 337 ACAATGACTTTGAGCCCTACCTTACTGAGGAGTCAATCAGAGTAAACAGTCCCTCAA 396
|
|
QY 121 TGAGCAGCCCTACCTTACTGAGGAGTCAATCAGAGTAAACAGTCCCTCAA 180
|
|
Db 397 TGAGCAGCCCTACCTTACTGAGGAGTCAATCAGAGTAAACAGTCCCTCAA 456
|
|
QY 181 ATGAGGCTCCGTGCTTACTGAGGAGTCAATCAGAGTAAACAGTCCCTCAA 239
|
|
Db 457 ATGAGGCTCCGTGCTTACTGAGGAGTCAATCAGAGTAAACAGTCCCTCAA 516
|
|
QY 240 CAGCTCAGTAAACGAGGAGTCAATCAGAGTAAACAGTCCCTCAA 299
|
|
Db 517 CAGCTCAGTAAACGAGGAGTCAATCAGAGTAAACAGTCCCTCAA 576
|
|
QY 300 CTGGGGAACAAATCTATCAGCAGAGTCAATCTTCTGAAACCCCTGCTTCTCA 359
|
|
Db 577 CTGGGGAACAAATCTATCAGCAGAGTCAATCTTCTGAAACCCCTGCTTCTCA 636
|
|
QY 360 GCAT-GGGGGACAAAGTGGGTCTCAAGGTACAGCAGCAGCAGCCTCTCCAGCA 417
|
|
Db 637 GCATGGGGGACAAAGTGGGTCTCAAGGTACAGCAGCAGCAGCCTCTCCAGCA 695
|
|
RESULT 66
AL580105/c 772 bp mRNA linear EST 16-FEB-2001
LOCUS
DEFINITION
AL580105 LTI_NFL008_Tc2 Homo sapiens cDNA clone CSODJ001YF07 3
prime, mRNA sequence.
ACCESSION
AL580105
VERSION
AL580105.1 GI:12945803
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 772)
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..772
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODJ001YF07"
/clone_lib="LTI_NFL008_Tc2"
/sex="male"
/tissue_type="T cells from T cell leukemia"
/notes="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 275 a 168 c 148 g 176 t 5 others
ORIGIN
Query Match 19.0%; Score 384.4; DB 9; Length 772;
Best Local Similarity 98.3%; Pred. No. 4.3e-72;
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Matches 395; Conservative 4; Mismatches 1; Indels 2; Gaps 1;
QY 1627 TTTTGTTCATTCTGATTTGTCATTTTATATCTGTATCGGTCTAAAGTGTCTAATTTTAC 1686
|
|
Db 772 TTTTGTTCATTCTGATTTGTCATTTTATATCTGTATCGGTCTAAAGTGTCTAATTTTAC 713
|
|
QY 1687 CCATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTT 1746
|
|
Db 712 CCATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTT 553
|
|
QY 1747 TTTTGTTCATTCTGATTTGTCATTTTATATCTGTATCGGTCTAAAGTGTCTAATTTTAC 1806
|
|
Db 652 TTTTGTTCATTCTGATTTGTCATTTTATATCTGTATCGGTCTAAAGTGTCTAATTTTAC 595
|
|
QY 1807 TCACGTCTCTGTCGTCGATTCGGGCTGGATGCTGTGTGGGGCATGATGTGTGGAGGAACGTG 1866
|
|
Db 594 TCACGTCTCTGTCGTCGATTCGGGCTGGATGCTGTGTGGGGCATGATGTGTGGAGGAACGTG 535
|
|
QY 1867 GAAGGTGCTTTAGGTCTGCTGCTCAGGCTCGGCGATCTTTTGTGTTGGCAGACACTTTTAA 1926
|
|
Db 534 GAAGGTGCTTTAGGTCTGCTGCTCAGGCTCGGCGATCTTTTGTGTTGGCAGACACTTTTAA 475
|
|
QY 1927 ATTTTACACTTTTCTTAAGAATTTCTAATGCCGTCTTAAGTTTATACCAATAATGCTG 1986
|
|
Db 474 ATTTTACACTTTTCTTAAGAATTTCTAATGCCGTCTTAAGTTTATACCAATAATGCTG 415
|
|
QY 1987 AGCTTTAAGTGTAGGATCTGCTAGTACAGACAGTGTGATGGA 2028
|
|
Db 414 AGCTTTAAGTGTAGGATCTGCTAGTACAGACAGTGTGATGGA 373
|
|
RESULT 67
BI283897/c 649 bp mRNA linear EST 19-JUL-2001
LOCUS
DEFINITION
UI-R-CX0s-ccx-h-11-0-UI-s1 UI-R-CX0s Rattus norvegicus cDNA clone
UI-R-CX0s-ccx-h-11-0-UI 3', mRNA sequence.
ACCESSION
BI283897
VERSION
BI283897.1 GI:14936090
KEYWORDS
EST.
SOURCE
Norway rat.
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 649)
Bonaldo, M.P., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
non-normalized rat placenta pool library cDNA Library Preparation:
M.B. Soares Lab Clome distribution: clones will be available
through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1..649
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CX0s-ccx-h-11-0-UI"
FEATURES
source
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/clone_lib="UI-R-CX0s"
/dev_host="ADULT"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: p773b-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CX0s
library is a non-normalized library constructed from the
following rat placenta tissues: embryonic day 17,
embryonic day 19, embryonic day 21. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=UI-R-CX0s
TAG_TISSUE=rat placenta pool
TAG_SEQ=TCACGACGT"

BASE COUNT 180 a 162 c 120 g 187 t
ORIGIN

Query Match 18.9%; Score 383.8; DB 13; Length 649;
Best Local Similarity 80.9%; Pred. No. 5.9e-72;
Matches 514; Conservative 0; Mismatches 102; Indels 19; Gaps 5;

Qy 771 CCGCTGCATGACGACCAAGGCGCGTCTACTGCTCTTCAGCGTCAATGGAGTGGGCA 830
Db 649 CCGCTCCATGACGACCAAGG--CCTGTATTCTTCTTCTAGTGTCAATGGAGTGGACA 592
Qy 831 TTTTGTGGGTGGCCGAGATGAGTCCCGTGGTACCGGACCGACCGTGGCGGTCTG 890
Db 591 TTTCTGTGGGTGGCAGAAATGAAGTCCCGTGGTACCGGACCGTGGCGGTCTG 532
Qy 891 GTCTCAGGACCAAGTGGAGGGAAGTTTGATGTCAGTGGATTTTTGTAAAGGATGTACC 950
Db 531 GTCTCAGGACCAAGTGGAGGGAAGTTTGATGAGTGGATTTTTGTCAAGGATGTGCC 472
Qy 951 CAATAACAGCTCCGGCAGATCAGGCTGGAGTAACGACAAACAAACCGGTGCACAACTC 1010
Db 471 CAATAATCAACTGGCGCAGATCAGACTGGAGTAACGACAAACAAACCGCTGTCAAACTC 412
Qy 1011 CCGGACACCCAGGAGTGCCCTTAGAAACCAAGCAAGTGTGTAATATATCAGTTC 1070
Db 411 CCGTGACACCGAGGAGTGCCCTTAGAAACCAAGCAAGTGTGTAATATATGCGTC 352
Qy 1071 CTACAAGCACAACTCCATCTTCGACGACTTTGCTCACTACGAGAGCGCCA-GAGGA 1129
Db 351 CTATAAGCACAACTCCATCTTTGACGACTTTTCTCATTTATGAGAGCGCCAGGAGA 292
Qy 1130 GGAGAGGTGTGGCAAGGAACGCGCAGTGCAGAAACAAACATGAGGGCGAACCGATTT 1189
Db 291 AGAGGAGGTAGTGGCAAGGAAGGAGCAATCGAAACAAACAAATAGGACGCGGTTT 232
Qy 1190 CTTACATGTTCTAACGTTTGACTTTGAAACACAGTTTAAACACAGTGTGCTGCAGCT- 1248
Db 231 GTTTTGTGTTAATGGTTGACTTTGAAACACAGTTTAAACGCTGTATGCTGGTGTCTC 172
Qy 1249 -----CCAGTGTGTCGTCGCGCGGGGTTGAGTGTGTCATCTTTGCGCTTTCTT 1298
Db 171 TCCGAGTCAGTCCAGTGTGCTGCTCGTGGGGTTAATGTTGCACTTTATCTTTGTA 112
Qy 1299 GTCGTTGATTTTTCGCCAGATGAGTCTGCATTTATTTGATCTTTTCTATGATATAAT 1358
Db 111 G-...TTCAATTTTTCAGATGAGTCTGCATTTCAATTTGTA-TTTTCTATGATATAAT 57
Qy 1359 CCTGTAGAAGTCACTAATAAAGGAGTATTTTTTT 1393
Db 56 ATTGTAGAAGTCACTAATAAAGGAGTATTTTGT 22

RESULT 68
BI662159 862 bp mRNA linear EST 12-SEP-2001
LOCUS 60305178F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5350818 5',
DEFINITION mRNA sequence.
```

ACCESSION BI662159
VERSION BI662159.1
KEYWORDS GI:15576395
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 862)
AUTHORS NTH-NGC http://ngc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LAM11891 row: 1 column: 19
High quality sequence stop: 861.
Location/Qualifiers
1..862
/organism="Mus musculus"
/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:5350818"
/clone_lib="NCI_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."

BASE COUNT 249 a 167 c 177 g 269 t
ORIGIN

Query Match 18.5%; Score 374.4; DB 13; Length 862;
Best Local Similarity 74.1%; Pred. No. 5.9e-70;
Matches 562; Conservative 0; Mismatches 171; Indels 25; Gaps 6;

Qy 844 GCCGAGATGAATCCCGCTGGACTACGGACCAAGTCCGGGTCTGCTCAGGACAAG 903
Db 1 GCAGAGATGAATCCCGCTGGACTACGGACCAAGTCCGGGTCTGCTCAGGACAAG 60
Qy 904 TGGAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGATGTACCAATAACAGCTC 963
Db 61 TGGAGGGGAAGTTTGATGTGAAGTGGATTTTGTGAAGATGTGCCCAACACAGCTG 120
Qy 964 CGGCACATCAGCTGGAGATAACGACAAACAACTCTGCACAACTCCCGTGATACAG 180
Db 121 CGGCACATCAGCTGGAGATAACGACAAACAACTCTGCACAACTCCCGTGATACAG 180
Qy 1024 GAGTGGCCCTTAGAAAAAGCCAGCAAGTGTGTAATATATCAGTCTCTCAAGCACACA 1083
Db 181 GAGTGGCCCTTAGAAAAAGCAAAACAAAGTGTGTAAGATTTATCGCTTCTATAAGCACACA 240
Qy 1084 ACCTCCATCTTCAGACGACTTTGCTCACTACGAGAGGCCCA-GAGGAGGAGGAGTGGT 1142
Db 241 ACCTCTATCTTTGACGACTTTTCTCATTTAGAAAGCCCGAGGAGGAGGAGTGGT 300
Qy 1143 CGCAAGGAACGCGAGTTCGAAACAAACAAATGAGGGGGAACACAGTTTCTTACATGTTCTA 1202
Db 301 CGTAAGGAAGACAGATTCGAAACAAACAAATGAGAAACAGCCAGTTTGTGTTGTTAAT 360
Qy 1203 ACCTTTCATCTTTGAAACAGTTTAAACACAGTGTGCTGTGTCAGCT-----CCA 1251
Db 361 GGTGACTTTGAAACACAGAGTTTAAAGCTGTATGCTTGGTGTCTCAGGAGTCACTC 420

QY 1252 GTGTGTCGTCCTCGGGGTTGAGTGTGCACTTTGCTTCTTGTGCTGATTTT 1311
|||||
Db 421 CAGTGTGCTCGTGGGGTTGATTTGTCATCTTTATCTTTGTAG---TTCAATTT 476
|||||
QY 1312 GCCAGATGATCTGATTTATTTGTTACTTTTCTATGATTAATATCCCTGTAGAAGTCA 1371
|||||
Db 477 TGCAGATGATCTGATCTCAATTTGA-TTTTCTATGATTAATATTTGTAGAAGTCA 535
|||||
QY 1372 CTAATAAAGAGTATTTTCTGTCAGCTTATCAATCAGACGATCTAATGTGAATGT 1431
|||||
Db 536 CTAATAAAGAGTA--TTCTGTTGTAGCTTATCAGTCAGATTTGACCTAATGCATAATAT 593
|||||
QY 1432 AGTATCTCTTAAAAACAAGCATCTATTTTGGCAGAAATGTCTTAAATTCAGTCAT 1491
|||||
Db 594 AAATAATCTTCAAAACAACACCTAATACATCCCAAGATAATTT-----TTATTTGG 647
|||||
QY 1492 TTGATATCTGTGAGACTTCTATATTTCTCATCTCTTATTTGCTTTTGTAGCAACATAGA 1551
|||||
Db 648 CAGAAATTAATGTTCTTATCTTATATCTAGCCATTTAATATCCCTATAGGATATTTTCA 707
|||||
QY 1552 AACCATGAGTCATTTTGTCTATTTAGAGTATTTCTGTATAA 1589
|||||
Db 708 TGCTTTGCTCTCTCTGCTTTTACGCAACAAACAAA 745
|||||

RESULT 69

BM775261/c

LOCUS

DEFINITION fy39a07.x1 Sugano SJD adult male Danio rerio cDNA clone 5602069 3' similar to TR:Q9Y5A9 Q9Y5A9 NY-REN-2 ANTIGEN. ; mRNA sequence.

ACCESSION BM775261

VERSION

BM775261.1 GI:19104875

KEYWORDS

SOURCE

ORGANISM

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes

; Cyprinidae; Danio.

1 (bases 1 to 608)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy

, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood

, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,

Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,

Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.

and Wilson, R.

WashU Zebrafish EST Project 1998

Unpublished (1998)

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrfish@wustl.edu

Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA

Sequencing by: Washington University Genome Sequencing Center Clone

distribution information can be found through the I.M.A.G.E.

Consortium/LLNL send email to: info@image.llnl.gov

Seq primer: T7 from Gibco

High quality sequence stop: 472.

Location/Qualifiers

1. .608

/organism="Danio rerio"

/db_xref="taxon:7955"

/clone_lib="5602069"

/sex="male"

/tissue type="whole body"

/dev stage="adult"

/lab_host="DH10B (phage resistant)"

/notes="vector: pME18S-FL3; Site 1: DraIII (CACCATGTG);

Site 2: DraIII (CAGTGTGTG); 1st strand cDNA was primed

with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTTTTTTTT];

double-stranded cDNA was ligated to a DraIII adaptor [GTGGCTACTGG], digested and cloned into distinct DraIII site of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed and donated by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAGCTCG and 3' end primer CGACCTGCAGCTCGAGACA."

BASE COUNT 115 a 167 c 161 g 165 t

ORIGIN

Query Match 17.9%; Score 363.8; DB 14; Length 608;

Best Local Similarity 79.6%; Pred. No. 1.1e-67;

Matches 442; Conservative 0; Mismatches 112; Indels 1; Gaps 1;

QY 604 AACTGAAGCGTCTCACAGCTACACCCGAAAGAGCTTTGAGTGGAACTCTGAAAGCGGG 663

Db 608 AAGTCGTCGCGGCACACAGCTACAAACCCCAAGAGGATTCGATTGGAAACCTGAAAAATGGC 549

QY 664 CGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGACATCCACGCTCCATTTAAGTACTCC 723

Db 548 CGGTGTTTCATCATTTAAGAGCTACTCTGAGGACGAGCTCCATCGCTCCATCAAGTACTCC 489

QY 724 ATCTGTGTAGCACAGACGACGCAACAAAGCGCTTGAAGCGCTTCCGCTGCATGAGC 783

Db 488 ATCTGTGTAGCACGACGCAACAAAGCGCTTGAAGCGCTTCCGCTGCATCAAC 429

QY 784 AGCAAGCGGCGCGTCTACCTGCTCTTACGCGTCAATGGGAGTGGGCAATTTTGTGGGTG 843

Db 428 GCAAAAGGTCCTGCTTACCTGCTTTCAGCGTCAACGCGGAGGACACTTCTGTGGCGTG 369

QY 844 GCGGAGATGAAGTCCCGCTGGAGTACGCGCAGGTCGCGGGGTCTGGTCTCAGGACAAG 903

Db 368 GCGGAGATGCGTTCGCTGTAGACTAGGACGAGTCCCGGTGTTGGGCGGAGGACAAG 309

QY 904 TGAAGGCGGAAGTTTGATGTCCAGTGGATTTTGTTAAGGATGTACCCCAATAACCAAGCTC 963

Db 308 TGAAGGCGCAAAATTTGATGTGGAGTGGCTGTTTGTAAAGACGTGCCCAACAGTCAGCTC 249

QY 964 CGGCACATCAGGCTGAGAAATACGACAAACACCGGTACAACTCCCGGGACACCCAG 1023

Db 248 AGGCACATCCGCTGAGAAACATGACAAACGCGGTGACCACTCGCGTGCACACAG 189

QY 1024 GAGGTGCTTGAAGAAAGCAAGCAAGTGTCTGAAATTTATCAGTTCTCTACAAAGCACACA 1083

Db 188 GAGGTGCTTGAAGAAAGCAAGCAAGTGTCTGAAATTTATCAGTTCTCTACAAAGCACACA 129

QY 1084 ACCTCCATCTTCGACGACTTTTGTCTACTAGGAGAGCGCCA-CAGGAGGAGGAGGTGGTG 1142

Db 128 ACCTCCATCTTCGATGACTTCTCACATTACGAGAAACGCGCAGGAGGAGGAGGTGGTA 69

QY 1143 CGCAAGCAACGGCAG 1157

Db 68 AGAAGAATCTTCAG 54

RESULT 70

AW766504/c

LOCUS

DEFINITION da63d11.x1 Hartland stage 19-23 Xenopus laevis cDNA clone

IMAGE:3199605 3', similar to TR:O64526 O64526 YUPB12R.13 PROTEIN.

; mRNA sequence.

ACCESSION AW766504

VERSION AW766504.1 GI:7698494

KEYWORDS

SOURCE

ORGANISM

African clawed frog.

Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 659)

AUTHORS

Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.

TITLE
JOURNAL
COMMENT

WashU Xenopus EST project, 1999
Unpublished (1999)
Other ESTs: da63d11.y1

Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
Library constructed by R. Harland, PhD. (University of California, Berkeley)

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 503.

FEATURES

source

Location/Qualifiers
1. .659
/organism="Xenopus laevis"
/db_xref="taxon:8355"
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/tissue_type="neural"
/dev_stage="stage 19-23"
/lab_hosts="DH10B (phage-resistant)"
/note="vector: pCS107 (custom); Site 1: NotI; Site 2: SalI
; cDNA made by oligo-dT priming. Library constructed by
Dr. Francesca Mariani in the laboratory of R. Harland,
Ph.D. (University of California, Berkeley). References:
XBP-2 is a transcriptional repressor that converts
ectoderm into neural tissue. Mariani, FV. Harland, RM.,
Development. 1998 Dec;125(24):5019-31. PMID: 9811586; UI:
99030283; Use of large-scale expression cloning screens in
the xenopus laevis tadpole to identify gene function.
Grammer TC, Liu KJ, Mariani FV, Harland RM. Dev Biol.
2000 Dec 15;228(2):197-210. PMID: 11112324; UI: 20564075;
2000 Dec 15;228(2):197-210. PMID: 11112324; UI: 20564075;
Note: This is a Xenopus Gene Collection (XGC) library."

BASE COUNT

ORIGIN

Query Match 17.9%; Score 363; DB 10; Length 659;
Best Local Similarity 82.5%; Pred. No. 1.7e-67;
Matches 439; Conservative 0; Mismatches 91; Indels 2; Gaps 2;
QY 625 TACAACCCGAAGAGTTTGAAGTGAATCTGAAAGCGGCGTGTGTTTCATCATCAAGAGC 684
DB 659 TATAACCTTAGGATTTTGAAGTGAATCTGAAATGACCTGTGTTTATTAAGAGT 600
QY 685 TACTCTGAGGACGACATCCACCGCTCCATTAAAGTACTCCATCTCGTGTAGCAGAGCAC 744
DB 599 TATT-TGAGGATGATATCCCCNGTTCCATCATCATATTCCATTTGGTGACGACAGCAT 541
QY 745 GGCAACAGCGCTGGACAGCGCTTCGGCTGCATGACGACAGGCGGCGTCTACCTG 804
DB 540 GGGAAATAACCGCTTGGATTAACGCTTTTCGGCTCCATGAATGCAAGGCGGCGTCTACCT 481
QY 805 CTCCTTACGCGTCAATGGAGTGGGCAATTTTGTGGGTGGCGGAGATGAAGTCCCGGTG 864
DB 480 CTGTTACGCGTCAACGCGAGTGGACATTTTTCGGCGTAGCCGAGATGAAGTCCCGGTG 421
QY 865 GACTACGGCACAGTGGCGGGGTCTGTGCTCAGGACAGTGGAAAGGGGAAGTTTGTGTC 924
DB 420 GACTATGGCACAGTGGCGGGGTCTGTGCTCAGGACAAATGGAAGGGCAAGTTTGACGTC 361
QY 925 CAGTGGGATTTTGTAGGATGTACCCAAATACAGCTCCCGGCACATCAGGCTGGAGAT 984
DB 360 AAGTGGCTCTTTGTCAAGGAGCGTTCCCAACCAACAGCTGAGGCGACATCCCGCTGGAGAT 301

QY 985 AACGACAAACACCGGTGCACAACTCCCGGACACCCAGGAGTGCCTTAGAAAAAGCC 1044
DB 300 AACGACAAACACCGGTGCACAACTCCCGGACACCGGAGGTGCCCTTAGAAAAAGCA 241
QY 1045 AAGCAAGTGTGAAAAATATCAGTTCCTTCAAGCACACCACTCCATCTTCGAGACTTT 1104
DB 240 AAACCTGGTGTCTAAATATCATTTGCCACTTTACAAGCACACGACCTCCATCTTTGATGACTTT 181
QY 1105 GCTCACTACGAGAGACGCCA-GAGGAGGAGGAGGTGGTGGCAAGGAGACGCG 1155
DB 180 TCTCATTACGAGAAAGCGCGCAGGAAGAGAGGTGTGTGCCCAAGGTAACGC 129

RESULT 71
BI254326
LOCUS
DEFINITION BI254326 733 bp mRNA linear EST 17-JUL-2001
602976619F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5115652 5',
mRNA sequence.
ACCESSION BI254326
VERSION
KEYWORDS BI254326.1 GI:14806626
SOURCE EST.
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 733)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11281 row: f column: 05
High quality sequence stop: 693.
Location/Qualifiers
1. .733
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/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

BASE COUNT 176 a 234 c 200 g 123 t
ORIGIN

Query Match 17.9%; Score 362.6; DB 13; Length 733;
Best Local Similarity 97.3%; Pred. No. 2e-67;
Matches 390; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
QY 400 GCTCAGGCTCTCCAGCACAGCCCCCAGCTTTGGCTCAACCGCAGTATCAAGAGCCCTCAG 459
DB 333 GCTCAGGCTCTCCAGCACAGCCCCCAGCTTTGGCTCAACCGCAGTATCAAGAGCCCTCAG 392
QY 460 CAGCACCCAGACCCCGCTGGTTGCCCGCAGCAGCAAGAACCGCGGGGTTTGGCGAGGC 519
DB 393 CAGCACCCAGACCCCGCTGGTTGCCCGCAGCAGCAAGAACCGCGGGGTTTGGCGAGGC 452
QY 520 GGAGGGCTGGCAGCGATAGCACTCTCTGGAAACGCTCCAGCCTAATTTCTGCCCGCCAGC 579
DB 453 GGAGGGCTGGCAGCGATAGCACTCTCTGGAAACGCTCCAGCCTAATTTCTGCCCGCCAGC 512
QY 580 GTCGAATCCCAACCCCGCTCTTTGAAAAAAGCTGAAGGCTGCTCACAGCTACAAACCCGAAAGAG 639

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Db 513 GTGGAATCCACCCCTGCTTGAACAACCTGAAGGCTGCTCACAGCTACCAACCCGAAAGAG 572
Qy 640 TTTGAGTGAATCTGAAAGCGGGCGTGTTCATCATCAAGAGCTACTCTGAGGACGAC 699
Db 573 TTTGAGTGAATCTGAAAGCGGGCGTGTTCATCATCAAGAGCTACTCTGAGGACGAC 632
Qy 700 ATCCACCGCTCCATTAAAGTACTCCATCTGGTGTAGCAGAGCACGGCAACAGCCCTG 759
Db 633 ATCCACCGCTCCATTAAAGTACTCCATCTGGTGTAGCAGAGCACGGC-ACAAGCGCTG 691
Qy 760 GACAGCGCTTCGCTGCATGACGACGACGAGGCGCGTCTA 800
Db 692 GACAG-GCCTTCGCTGCATGAGCGCAAGGGGCGCGTCTA 731

RESULT 72
BES42677
LOCUS BES42677
DEFINITION 601067173F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453235 5',
mRNA sequence.
ACCESSION BES42677
VERSION BES42677.1 GI:9771322
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM8436 row: b column: 20
High quality sequence stop: 632.
Location/Qualifiers
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/cell_line="WGC36"
/lab_host="DH10B"
/notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
BASE COUNT 187 a 222 c 226 g 155 t
ORIGIN
Query Match 17.8%; Score 361.8; DB 10; Length 790;
Best Local Similarity 97.7%; Pred. No. 3e-67;
Matches 388; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

Qy 23 ACAAATGGTTTCGTTACATCAGAGGATACAGTTTCATGACAATGACTTTTCAGCGCTACCT 82
Db 1 ACAAATGGTTTCGTTACATCAGAGGATACAGTTTCATGACAATGACTTTTCAGCGCTACCT 60
Qy 83 TACTGGACAGTCAATCAGAGTAACTACCTTACCTCAATGAGGACCCCTACCTGTCCAG 142
Db 61 TACTGGACAGTCAATCAGAGTAACTACCTTACCTCAATGAGGACCCCTACCTGTCCAG 120
Qy 143 CTATTACCCCGCGTCCATTGGATTTCCTTACTCCCTCAATGAGGCTCCGTGGTCTACTGC 202
Db 121 CTATTACCCCGCGTCCAGTGGATTTCCTTACTCCCTCAATGAGGCTCCGTGGTCTACTGC 180

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Qy 203 AGGGAGCCCTCCGATTCATACCTCACCACTTACGGA-CAGCTCAGTAAACGAGACCATC 261
Db 181 AGGGAGCCCTCCGATTCATACCTCACCACTTACGGA-CAGCTCAGTAAACGAGACCATC 240
Qy 262 ATTATTATG-CAGATGCTGTTTTCGGGAGCGCTGGGGCGCTGGGGAACAACATCTATCAG 320
Db 241 ATTATTATGTCAGATGCTGTTTTCGGGAGCGCTGGGGCGCTGGGGAACAACATCTATCAG 300
Qy 321 CACAGGTTCAATTTTTCCTCAAAACCTCGGTTCTCAGCATGGGGGACAAAGTGGGTCT 380
Db 301 CACAGGTTCAATTTTTCCTCAAAACCTCGGTTCTCAGCATGGGGGACAAAGTGGGTCT 360
Qy 381 CAAAGTTCAGCAGACCCAGAGCTCAGCTTCCACGCA 417
Db 361 CAAAGTTCAGCAGACCCAGAGCTCCGCGTATGGAGCA 397

RESULT 73
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LOCUS BFO25564
DEFINITION dg06d04.x1 Xenopus laevis gastrula non normalized Xenopus laevis
cDNA clone XENOPUS SOURCE_ID:xlnga002n08 3' similar to TR:Q9Y5A9
Q9Y5A9 NY-REN-2 ANTIGEN.; mRNA sequence.
ACCESSION BFO25564
VERSION BFO25564.1 GI:10755991
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 674)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
WashU Xenopus EST project, 1999
Unpublished (1999)
Other ESTs: dg06d04.y1
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 458.
Location/Qualifiers
1. .674
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/db_xref="taxon:8355"
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/clone_lib="Xenopus laevis gastrula non normalized"
/tissue_type="gastrula (stages 10.5, 11.5 mixed)"
/lab_host="Top-10 F'"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from 2ug of Poly A+ RNA (equal
parts from stage 10.5 and stage 11.5 gastrulae).
EcoRI-XhoI cut cDNA was then ligated into Unizap-XR
(Stratagene) with EcoRI at the 5' end and XhoI at the 3'
end. SS-library phagemids were prepared by mass excision
from the original library and normalized by hybridization
to biotinylated driver (prepared from the same library by
PCR) to Cot-omega of 11. After removal of hybrids and
excess driver by streptavidin sepharose chromatography,
the ss-phagemids were made double stranded and

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ACCESSION   BM828295
VERSION     BM828295.1  GI:19184704
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 361)
AUTHORS    Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE      21C Frontier Korean EST Project 2001
JOURNAL     Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 111 row: B column: 10
            High quality sequence stop: 361.

FEATURES             Location/Qualifiers
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                     /sex="F"
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                     /cell_line="SNU-16"
                     /lab_host="DH10B"
                     /note="Organ: Stomach; Vector: pT7T3-Pac; Site 1: EcoRI;
                     Site 2: NotI; The S22SNU16 library was contributed by the
                     Soares laboratory and it was constructed as described by
                     Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
                     Research 6 (9): 791-806. RNA was prepared from harvested
                     cells of SNU-16 culture. SNU-16 cell was obtained from
                     Korean Cell Line Bank (KCLB). SNU-16 was established from
                     ascitic fluids of Korean patients by Park J.G. et al.
                     (1990), Cancer Res 50: 2773-2780."
BASE COUNT   78 a 66 c 71 g 146 t
ORIGIN
Query Match      17.3%; Score 351.4; DB 14; Length 361;
Best Local Similarity 98.3%; Pred. No. 5.5e-65;
Matches 355; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1605 CTGAATCAAAAGGTTAATGATTTTGTTCATTCTGATTTGTTCATTATTATTCGTGA 1664
DB 1 CTGAATCAAAAGGTTAATGATTTTGTTCATTCTGATTTGTTCATTATTATTCGTGA 60
QY 1665 TCGGTCTAAAGTGCTAATTTACCACTTGTGATTTTTCGTAGACAGATACTTTTAATTT 1724
DB 61 TCGGTCTAAAGTGCTAATTTACCACTTGTGATTTTTCGTAGACAGATACTTTTAATTT 120
QY 1725 TTCAAATTTGGCAGACACTTTTTCCTTTCGAAATCTTTCCTTCCAGATCTGTTC 1784
DB 121 TTCAAATTTGGCAGACACTTTTTCCTTTCGAAATCTTTCCTTCCAGATCTGTTC 180
QY 1785 CCACTGAACAGCCCGTCCCTCCTGCTGCTGTCCTGTCCTGATTTGGGCTGGATGTTGG 1844
DB 181 CCACTGAACAGCCCGTCCCTCCTGCTGCTGTCCTGATTTGGGCTGGATGTTGG 240
QY 1845 GGCATGATGTGTGGAGGAATCGGAAGGTGCTTTAGGTCTGGTTTCAGGGTCGGGCACTTT 1904
DB 241 GGCATGATGTGTGGAGGAATCGGAAGGTGCTTTAGGTCTGGTTTCAGGGTCGGGCACTTT 300
QY 1905 TGTGTTTGACATCTTTTAAATTTTACACCTTTTCTTAAGAAATCTTAATGCGGCTTA 1964
DB 301 TGTGTTTGACATCTTTTAAATTTTACACCTTTTGGCTTGAAGAAATCTTAATGCGGCTTA 360

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QY 1965 A 1965
DB 361 A 361

RESULT 76
BE715628/c
LOCUS      BE715628
DEFINITION CM3-HT0745-150600-213-a04 HT0745 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE715628
VERSION   BE715628.1  GI:10103893
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 373)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE    20202663
COMMENT    Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=4t2=CM3-HT0745-150
            600-213-a04&t3=2000-06-15&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 14
            High quality sequence stop: 371.

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                     /dev_stage="Adult"
                     /note="Organ: head neck; Vector: puc18; Site_1: SmaI;
                     Site 2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT   83 a 109 c 92 g 89 t
ORIGIN
Query Match      17.3%; Score 350.8; DB 12; Length 373;
Best Local Similarity 99.2%; Pred. No. 7.4e-65;
Matches 363; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 626 ACAACCCGAAAGTTTGAGTGGATCTGAAAGCGGGGTGTGTTTCATCATCAAGAGCT 685
DB 372 ACAACCCGAAAGTTTGAGTGGATCTGAAAGCGGGGTGTGTTTCATCATCAAGAGCT 313
QY 686 ACTCTGAGGACGACATCCACCGCTCCATTAAAGTACTCCATCTGGTGTAGCAGACGACG 745
DB 312 ACTCTGAGGACGACATCCACCGCTCCATTAAAGTACTCCATCTGGTGTAGCAGACGACG 253
QY 746 GCACAAAGCGCTGGACAGCGCTTCGGCTGCATGACGACGAGGGGCCGCTCACTGCG 805
DB 252 GCACAAAGCGCTGGACAGCGCTTCGGCTGCATGACGACGAGGGGCCGCTCACTGCG 193

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for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library.

BASE COUNT	134 A	241 C	200 G	126 T
ORIGIN				
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Best Local Similarity	99.5%; Pred. No. 1.2e-63;			
Matches 367; Conservative	0; Mismatches 0; Indels 2; Gaps 2;			
Qy	1	CAAAAGCACAAGTAATAAAGTACAAAATGGTTGCTTACATCAGAAGATACAGATTCAATG	60	
Db	331	CAAAAGCACAAGTAATAAAGTACAAAATGGTTGCTTACATCAGAAGATACAGATTCAATG	390	
Qy	61	ACAATGACTTTTGAGCCCTACCTTACTTGGACAGTCCAAATCAGAGTAAACAGTTACCCTCAA	120	
Db	391	ACAATGACTTTTGAGCCCTACCTTACTTGGACAGTCCAAATCAGAGTAAACAGTTACCCTCAA	450	
Qy	121	TGAGCACCCCTACCTGTCCAGTATATACCGCCGCTCATTTGGATTTCCTTACTCCCTCA	180	
Db	451	TGAGCACCCCTACCTGTCCAGTATATACCGCCGCTCATTTGGATTTCCTTACTCCCTCA	510	
Qy	181	ATGAGGCTCCGTGGTCTACTGCAGGGGACCTCCGATTCATACCTCACCACCTACGGAC	240	
Db	511	ATGAGGCTCCGTGGTCTACTGCAGGGGACCTCCGATTCATACCTCACCACCTACGGAC	570	
Qy	241	AGCTCAGTAACGAGAACCATCATTTTTATGCACGATGCTGTTTTTGGCAGCCTGGGGGCC	300	
Db	571	AGCTCAGTAACGAGAACCATCATTTTTATGCACGATGCTGTTTTTGGCAGCCTGGGGGCC	629	
Qy	301	TGGGGAACCAACATCTATCATGACAGTTCATTTTTTCCCTG-AAAACCTTCGTTCTCA	359	
Db	630	TGGGGAACCAACATCTATCATGACAGTTCATTTTTTCCCTGAAAAACCTTCGTTCTCA	689	
Qy	360	GCATGGGGG 368		
Db	690	GCATGGGGG 698		
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BB610489	1010 bp mRNA linear EST 26-OCT-2000			
LOCUS	musculus cDNA clone Z210410K23 5', mRNA sequence.			
DEFINITION	BB610489 RIKEN full-length enriched, adult male stomach Mus			
VERSION	BB610489			
ACCESSION	BB610489			
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.A, Ishii,Y., Ito,M., Kawai,J., Konno,H., Koudou, Hiramoto,K., Horii,F., Miyazaki,A., Nomura,K., Ohno,M., M., Koya,S., Matsumura,T., Saito,R., Sakai,C., Sano,H., Sasak Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sano,H., Sasak D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001)			
TITLE	Unpublished (2001)			
JOURNAL	Contact: Yoshinori Hayashizaki			
COMMENT	Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugihara,Y., Shibata,K., Itoh M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.			

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsaura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.

Riken integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)

Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yananaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

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Location/Qualifiers
1..1010
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="2210410K23"
/clone_lib="RIKEN full-length enriched, adult male stomach"
/sex="male"
/tissue_type="stomach"
/dev_stage="adult"
/lab_host="SOLR"
/note="Site 1: XhoI; Site 2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGGAGCGCGCCGACCTGCAGTCTTTTTCCTTTTTCVN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGGAGATCTCGAGTTAATAATTAAATCCTCCCCCCC 3']. cDNA was cleaved with XhoI and SstI."
BASE COUNT      218 a   292 c   276 g    223 t       1 others
ORIGIN
Query Match          17.0%; Score 345; DB 10; Length 1010;
Best Local Similarity 89.2%; Pred. No. 1-2e-63;
Matches 372; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
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QY 1 CAAAAGCACAGAATAATAAGTACAAAATGGTTGGTTACATCAGAAGATACAGTTCAATG 60

Db 237 CAAAAGCACAGAATAATAAGTACAAAATGGTTCTTTGCCATCAGAAGATGACGATTCATG 296

QY 61 ACAATGACTTTTGACCCCTACCTTACTCGCAGTCAGTCAATCAGATTAACAGTTACCCTCAA 120

Db 297 ACAATGACTTTTGACCCCTACCTTCTCGCAGTCAGTCCAATCCGAGTAAACAGTTACCCTCGA 356

QY 121 TGAGCGACCCCTACCTGTCCAGCTATTACCGCGCGTCCATTGGATTTCTTACTCCCTCA 180

Db 357 TGAGTGATCTTACCTGTCCAGTTACTATCAACCATCAATGGATTTCTTACTCCCTCA 416

QY 181 ATGAGGCTCGGTGGTTACTGTCAGGGGACCCCTCGGATTTCATACCTCACCACTACGGAC 240

Db 417 GCGAGGCACCATGGTCCACTGCAGGGGACCCCTCCATCCCGTATCTCACTACCTATGGAC 476

QY 241 AGCTCAGTAACGGAGACATCATTTTATGACAGTAGTCTGTTTTGGGAGCGCTGGGGCC 300

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Db 477 AACTTAGTAATGGAGACCATCACTTCATGCATGATGCTGTTTTTTGGGAGCGCTGGGGTC 536
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Db 537 TGGGGAACAACATTTACAGCACAGGTTTAATTTTTTCCCTGAAACCCCTCGATTCTCAG 596
Qy 361 CATGGGGACAAGTGGGTCTCAAGTTCAGCAGACCCAGAGCTCAGCCTCTCCACGCA 417
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RESULT 80
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DEFINITION AGENCOURT 8861752 NCI CGAP Mam2 Mus musculus cDNA clone
IMAGE:6439636 5', mRNA sequence.
ACCESSION BQ927973
VERSION BQ927973.1 GI:22343004
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1041)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbe-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM3959 row: p column: 05
High quality sequence stop: 413.
FEATURES
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/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:6439636"
/clone_lib="NCI CGAP Mam2"
/tissue_type="tumor, biopsy sample"
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/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 202 a 355 c 280 g 204 t
ORIGIN
Query Match 17.0%; Score 345; DB 14; Length 1041;
Best Local Similarity 89.2%; Pred. No. 1.2e-63;
Matches 372; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
Qy 1 CAAAGGACAGATAATAAGTACAAATGGTTGTTACATCAGAGGATACAGTTTCATG 60
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Qy 61 ACAATGACTTTGAGCGCTTACTTGACAGAGTCAAAATCAGAGTAACAGTTACCCCTCAA 120
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Qy 301 TGGGGAACAACATCTATCAGCACAGGTTCAATTTTTTCCCTGAAACCCCTCGGTTCTCAG 360
Db 328 TGGGGAACAACATTTACAGCACAGGTTTAATTTTTTCCCTGAAACCCCTCGATTCTCAG 387
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RESULT 81
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LOCUS BQ061839 720 bp mRNA linear EST 07-DEC-2001
DEFINITION laevis cDNA clone XL074d11 5', mRNA sequence.
ACCESSION BQ061839
VERSION BQ061839.1 GI:17423904
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 720)
REFERENCE Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
AUTHORS Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tehini@genes.nig.ac.jp.
FEATURES
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/clone="XL074d11"
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/tissue_type="whole embryo"
/dev_stage="stage 25"
/notes="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Mellcome/CRC Institute)."
BASE COUNT 230 a 135 c 158 g 197 t
ORIGIN
Query Match 16.9%; Score 342.8; DB 13; Length 720;
Best Local Similarity 71.9%; Pred. No. 3.6e-63;
Matches 476; Conservative 0; Mismatches 182; Indels 4; Gaps 2;
Qy 568 TCTGCCCCAGCGTCGAATCCACCCCGTCTTTGAAAAAACTGAAGGCTGTCTACAGCTAC 627
Db 14 TTTGCCCTTCGTTGTTGAAGTGACCCAGTACTGGAGAACTGMAAGGCCATTAAACAATAC 73
Qy 628 AACCCGAAAGATTGAGTGGATCTGAAAAGCGGGCGTGTTCATCATCATCAGAGCTAC 687
Db 74 AATCCCAAGACTTTTGACTGGAGTCTAAAAAATGACGAGTGTTTATATCATCAGAGCTAC 133
Qy 688 TCTGAGGACGACATCCACCGCTCCCAATTAAGTACTTCCATCTGGGTAGCAGACAGCAGGC 747
Db 134 TCTGAGACGATATTTCATCGTTCTATAAAGTACTCAATCTGGTGTAGCAGCAGACATGGC 193
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QY 748 AACAGGCGCTGGACAGCGCTTCCGCTGATGAGCAGCAAGGGGCCGCTACCTGCTC 807
D 194 AATAAAGCTTTGGATGCTGCTTACCGATCTTTGAATGGAAGGCCACCTTTATTTACT 253
QY 808 TTGAGGCTCAATCGGAGTGGGCAATTTTGGGGTGGCCGAGATGAAGTCCCGTGGAC 867
D 254 TTGAGGCTCAATCGGAGTGGGCAATTTTGGGGTGGCCGAGATGAAGTCCCGTGGAC 313
QY 868 TAGCGCACCAAGTGC CGGGGTCTGCTCTCAGGCAAGTGGAGGGGAAGTTTGTATGCCAG 927
D 314 TATAATGCTTATGCTGGAGTCTGGTCCGAGCAAAATGGAAGGGAAGTTTGTATGAAA 373
QY 928 TGGATTTTGTAAAGATGATACCAATACACAGCTCCGCGACATCAGGCTGGAGATAAC 987
D 374 TGGGCGCTTTGTCAAAGAGCTACCTAATAACAGTTCGGCATATTCGTTTGAAGAAATAAC 433
QY 988 GACACAAACCGGTGACAAATCCCGGGACACAGGAGGTGCGCTTAGAAAAGCCAAAG 1047
D 434 GATAACCAAGCTGTATCAACTCAAGGGACACTCAAGAGGTTCCTTAGAAAAGGCCAAG 493
QY 1048 CAAGTGTGAAAAATTTACAGTTCTTACAAGCACACAACTCCATCTTTCGACGACTTTGCT 1107
D 494 CAGATTTCTTAAATAATTTGCAATGCTTCAAGCATACAACTCTATCTTTGATGACTTTGCA 553
QY 1108 CACTACGAGAACCG-CCAGAGGAGGAGAGGTGTGCGCAAGGAACCGCAGAGTCGAAAC 1166
D 554 CATTATGAGAAGCGTCAAGAGGAGGAGGAGCCATGCGTAGGGA---GCGAAATCGAAAC 610
QY 1167 AACAATGAGGGCGAACAGTTTCTTACATGTTCTTACAGTTTTCAGTTTGAACAGTTTA 1226
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DEFINITION
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ACCESSION
  BJ064834
VERSION
  BJ064834.1 GI:17480195
KEYWORDS
  EST.
SOURCE
  African clawed frog.
ORGANISM
  Xenopus laevis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
  Xenopodinae; Xenopus.
REFERENCE
  1 (bases 1 to 706)
  Kitayama,A., Terabe,A., Mochii,M., Ueno,N., Shin-i,T. and Kohara
  Y.
  Expressed genes in X. laevis embryo
  Unpublished (2001)
  Contact: Tadasi Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.
  Location/Qualifiers
    1..706
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      /notes="vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
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according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute). "
BASE COUNT 224 a 130 c 157 g 195 t
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Query Match 16.9%; Score 342.2; DB 13; Length 706;
Best Local Similarity 71.8%; Pred. No. 4.8e-63;
Matches 476; Conservative 0; Mismatches 183; Indels 4; Gaps 2;
QY 567 TTCTGCCCCAGCGTCCGAATCCACCCCGTCTTGAAAAAATGAAAGGCTGCTCACAGCTA 626
D 38 TTGCGCTTCTGGTTTGAAGTACACCCAGTACTGGAGAAATGAAAGGCCATTAACAATA 97
QY 627 CAAACCGAAAGAGTTTGAAGTGAATCTGAAAAAGCGGCGGTGTTTCATCATCAAGAGCTA 686
D 98 TAATCCCAAAGACTTTGAGCTGGAGTCTAAAAAATGACGCTGTTTATCATCAAGAGCTA 157
QY 687 CTCTGAGGAGCATCCACCGCTCCATTAAGTACTTCATCTGCTGTTAGCACAGCACGG 746
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QY 747 CAAACAGCGCTGACAGCGCTTCCGCTGCATGACGACCAAGGGCGCGCTCTACCTGCT 806
D 218 CAATAAACGTTTGGATGCTGCTTACCGATCTCTGAATGAAAGGCCACTTTTATTACT 277
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D 278 CTTTCAGTGAATGGAAGTGGACATTTTGTGCTGAGCTGAAATGAAGTCTGTTGGA 337
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QY 927 GTGGATTTTGTAAAGTGTACCCCAATACAGCTCCGCAATCAGGCTGCGAGATAA 986
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D 578 ACATTATGAGAGCGTCAAGAGGAGGAGCCATGCGTAGGGA---GAGAAATAGAAA 634
QY 1166 CAAACAATGAGGCGCAACCAAGTTTCTTACATGTTCTTAACGTTTGAACACAGTTT 1225
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D 695 AAA 697

RESULT 83
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LOCUS
DEFINITION
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  5', mRNA sequence.
ACCESSION
  BJ023830
VERSION
  BJ023830.1 GI:20405230
KEYWORDS
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SOURCE
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 883)
  NIH-MGC http://mgc.nci.nih.gov/.
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TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM3282 row: g column: 09
High quality sequence stop: 684.

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1. .883
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/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library." 4 others
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ORIGIN
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Best Local Similarity 74.6%; Pred. No. 1e-62;
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QY 583 GAATCCCAACCCCGCTTGGAAAACTGAAGGCTGCTACAGCTACAAACCCGAAAGATTT 642
DB 35 GAACCCCAACCCAGTGTGGAGAGCTTCGGTCCATTATACTATAACCCCAAGATTTT 94
QY 643 GAGTGGAACTTGAAGAAGCGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGACATC 702
DB 95 GACTGGAATCTGAACATATGCGCGGCTTTTCATCATTAAGAGCTACTCTGAGGACGATTT 154
QY 703 CACCGCTCATTAAGTACTCTGTTGTTAGCAGACAGACGCGCAACAGCGCTGGAC 762
DB 155 CACCGTTCCATTAAATGTAATTTGGTGCAGCAGACGATGTTAAACAGAGACTGGAT 214
QY 763 AGCGCTTCCGCTGCATGAGCAGCAAGGGCGGCTACCTGCTCTCAGCGTCAATGGG 822
DB 215 GCTGCTTATCGTTTCATGAACGGGAAAGGCCCGTTTACTTTTCACTGTTCAACGGC 274
QY 823 AGTGGGCATTTTGTGGGTTGGCCGAGATGAAGTCCCCCGTGGACTACGGCACCAGTGCC 882
DB 275 AGTGGACACTTCTGTGGCGTGGCAGAAATGAATCTGCTGTGGACTACAAACATGTGCA 334
QY 883 GGGCTGCTCTCAGGCAAGTGGAGGAAAGTTGATGCTCCAGTGGATTTTGTAAAG 942
DB 335 GGTGTGGTCCCAGGACAAATGAAGGGTCTGTTGATGTGAGTGGATTTTGTGAAG 394
QY 943 GATGTACCAATAACAGCTCCGGCAGCATCAGGTGGAGATAACGACAAACCCGGTC 1002
DB 395 GACGTTCCCATATAGCACTCGGACACATTCGCTAGAGAACACAGGATTAACCATGTG 454
QY 1003 ACAAACTCCGGGACACCCAGGAGTGCCCTTTAGAAAAAGCCAAAGCAAGTGCTGAAAAAT 1062
DB 455 ACCAACTCTAGGACACTCAGGAAGTGCTCTGGAAGAGGCTAAGCAGGTGTTGAAAAAT 514
QY 1063 ATCAGTTCCTACAGGACACAACTCCATCTTCGACGACTTTGCTCACTACGAGAGCGC 1122
DB 515 ATAGCCAGCTACAAGCACCACCTTCCCATTTTGTATGACTTCTCACACTATGAGAAACGC 574
QY 1123 C-AGAGGAGGAGGAGTGGTGGCAAGGAACGGCAGAGTGTGAAACAAACAA 1172
DB 575 CAAGAGGAGAGAAAGTGTAAAGAGGACGTCNAGTCTGTGGAAATAA 625

RESULT 84
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LOCUS
DEFINITION
CH230-163C17.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-163C17, DNA sequence.
BH353078
BH353078.1 GI:17283812
GSS.
SOURCE
Norway rat.
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 739)
AUTHORS
Zhao, S., Shetty, J., Shatsman, S., Teagave, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
OTHER GSSs: CH230-163C17.TJ
COMMENT
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@email.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 163 row: C column: 17
Seq primer: T7
Class: BAC ends.

FEATURES
source
1. .739
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/db_xref="taxon:10116"
/clone="CH230-163C17"
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/sex="Female"
/cell_type="Brain"
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CHORI-230 Rat (BN/SnHsd/MCW) BAC library produced by
Pieter de Jong"
BASE COUNT 198 a 169 c 138 g 234 t
ORIGIN
Query Match 16.7%; Score 339; DB 17; Length 739;
Best Local Similarity 70.3%; Pred. No. 2.3e-62;
Matches 483; Conservative 0; Mismatches 200; Indels 4; Gaps 2;
QY 469 CAGACCCGCTGGGGTTGCCCAACAGAAAACGCGCGCTTTGGGCGAGAGCGGAGGGCT 528
DB 708 CAGAACTGTTGGGTAGTCTCTCGGAATAGGGGAACCGGCTTCAACCAAGAACATGGAACA 649
QY 529 GGCAGCGATAGCAACTCTCTCTGGAAACGTCGAGCTTAATTTCTGCC---CCAGCGTCGAA 585
DB 648 GGCAGTGAAGAACTTTGGTTTGGTGTGTACCTGTAGTGTTCACCTTCTAGTGTAGAG 589
QY 586 TCCCAACCCCTCTTGAAGAACTGAAGGCTGCTCACAGCTACACCGAAGAGTTTGGAG 645
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QY 646 TGGAACTCTGAAAAAGCGGCGGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGACATCCAC 705
DB 528 TGGAACTCTGAAATGACCGTGTGTTTATTAATTAAGAGCTATTCTGAGGATGATATACAC 469
QY 706 CGTCCATTAAAGTACTCCATCTGTGTAGCAGAGCAGCGCAACAAAGCGCTGGACAGC 765

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QY 826 GGGCATTTTTGTGGGGGCGGAGATGAAGTCCCGCTGAGTACGACCAAGTGGCGGG 885
Db 348 GGCATATTTTGTGGAGTGGCTGAAATGAAGTCTGTTAGACTATAATGCTTATGCTGT 289
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Db 228 GTTCCCAATTAACCAATTAACACATATTCGCTAGAAATTAATGACAAACAGTAACC 169
QY 1006 AATCCCGGACACCCAGGAGTGCCTTAGAAAAAGCCAAAGTGTGAAAAATATC 1065
Db 168 AATCAAGACACTCAAGAAGTACCCTAGAAAAAGCAAGTGTCTAAAAATAAT 109
QY 1066 AGTCTCTACAGACACAACTCTATCTTCGACGACTTTGCTACTACGAGAGCG-CCA 1124
Db 108 GCTACTTTCAAGCACACACCTCAATCTTTGATGACTTTGACATTATGAAAAAGCGTCA 49
QY 1125 GAGGAGGAGGAGTGGTGGCCAAAGAA 1151
Db 48 GAGGAGGAGGAGGAGTGGAGGTA 22

RESULT 85
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LOCUS prime, mRNA sequence.
DEFINITION AL515909
VERSION AL515909.1 GI:12779402
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 917)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
CONTACT Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 917
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DA001YB18"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library is not normalized, but is the control for
the normalized libraries. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
Maryland 20850, USA Fax : (1) 301 610 8371 Email :
filiang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 174 a 274 c 228 g 206 t 35 others
```

ORIGIN

```
Query Match 16.7%; Score 338; DB 9; Length 917;
Best Local Similarity 88.8%; Pred. No. 3.8e-62;
Matches 366; Conservative 17; Mismatches 27; Indels 2; Gaps 2;

QY 1 CAAAAGGACAGATAATAAAGTACAAAATGGTTCGTATCATCAGAAGGATACAGTTTCATG 60
Db 278 CAAAAGGACAAATATAATWMTTACAAAATGGTTCGTATCATCATATGWTATATTTCAAT 337
QY 61 ACAATGACTTTTGAGCCCTACCTTACTGGCAGTCAATCAGAGTAACAGTTACCCCTCAA 120
Db 338 AYAATTAATTTTAKCTCTACCTTACTGGACATTAATTAATTAATTAATTAATTAATTA 337
QY 121 TGAGCAGCCCTACCTGTCCAGCTATTACCCGCGCTCAATTTGGATTTCCTTACTCCCTCA 180
Db 398 TTAGCTACCCCTACCTTTTCAGCTATTATTCGCTTTTATTTGGATTTCCTTACTCCCTCA 457
QY 181 ATGAGGCTCGTG-GTCTACTGAGGGGACCTCCCGATTCCATACCTCACCCTACGGA 239
Db 458 ATGAGGCTCGTGCTATTTCTGGTACCCCTCCGATTCCATACCTCACCCTACGGA 517
QY 240 CAGCTCAGTAAGCGAGACCATCATTTTATGCGAGTGTGTTTGGCGAGCTGGGGGC 299
Db 518 CAGCTCAGTAAGCGAGACCATCATTTTATGCGAGTGTGTTTGGCGAGCTGGGGGC 577
QY 300 CTGGGGAAACAAATCATCTATCAGCACAGTTCATTTTTCCTGAAACCCCTGGTCTCTCA 359
Db 578 CTGGGGAAACAAATCATCTATCAGCACAGTTCATTTTTCCTGAAACCCCTGGTCTCTCA 637
QY 360 GCAT-GGGGGACAAAGTGGTCTCAAGGTGAGAGCCAGAGCTCAGCTCT 410
Db 638 GCATGGGGGACAAAGTGGTGTTCAGGTGAGAGCCAGAGCTCGCGGTAT 689

RESULT 86
AA460050 355 bp mRNA linear EST 09-JUN-1997
LOCUS zx66c02.r1 Soares total fetus Nb2HF8.9w Homo sapiens cDNA clone
DEFINITION IMAGE:796418 5' similar to TR:G849195 G849195 CHROMOSOME IV COSMID
9481 ; mRNA sequence.
ACCESSION AA460050
VERSION AA460050.1 GI:2184934
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 355)
AUTHORS Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie
, T., Waterston, R., and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m3 rev2 ET from Amersham
High quality sequence stop: 325.
Location/Qualifiers
1. 355
/organism="Homo sapiens"
/db_xref="GDB:6040577"
/db_xref="taxon:9606"
/clone="IMAGE:796418"
/dev_stage="8-9 weeks"
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/lab_host="DH10B"
 /note="vector: pT773D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from pooled 8-9 week
 (total) fetus material with a Not I - oligo(dT) primer [5'
 TGTTACCAACTGAGTGGAGCGCGCTTAATTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT773 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 85 a 104 c 97 g 69 t
 ORIGIN

Query Match 16.6%; Score 336.8; DB 9; Length 355;
 Best Local Similarity 99.1%; Pred. No. 7.4e-62;
 Matches 349; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 519 CGGAGGGCTGGCAGGATAGCAACTCTCTGGAAACCTCCAGGCTAATTTGCCCCCAG 578
 Db 5 CGGAGGGCTGGCAGGATA-CAACTCTCTGGAAACCTCCAGGCTAATTTGCCCCCAG 63

Qy 579 CGTGCATCCACCCCGCTTGAATACTGAAGCTGCTCACAGCTACACCCGAAAGA 638
 Db 64 CGTGCATCCACCCCGCTTGAATACTGAAGCTGCTCACAGCTACACCCGAAAGA 123

Qy 639 GTTTGAGTGGAAATCTGAAAAGCGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGA 698
 Db 124 GTTTGAGTGGAAATCTGAAAAGCGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGA 183

Qy 699 CATCCACCGCTCCATTAAGTACTCATCTGTTGATGACACAGACGCGCAACAAGCGCCT 758
 Db 184 CATCCACCGCTCCATTAAGTACTCATCTGTTGATGACACAGACGCGCAACAAGCGCCT 243

Qy 759 GGACAGCGCTTCCGCTGCATGACAGCAAGGCGCGCTCTACCTGCTCTTCAGCGTCAA 818
 Db 244 GGACAGCGCTTCCGCTGCATGACAGCAAGGCGCGCTCTACCTGCTCTTCAGCGTCAA 303

Qy 819 TGGGAGTGGGCATTTTGTGGGGTGGCCGAGATGAAGTCCCGCGTGGACTAC 870
 Db 304 TGGGAGTGGGCATTTTGTGGGGTGGCCGAGATGAAGTCCCGCGTGGACTAC 355

RESULT 87
 BQ899696
 LOCUS
 DEFINITION AGENCOURT_8753787 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6393617
 5', mRNA sequence.

ACCESSION BQ899696
 VERSION BQ899696.1 GI:22291698
 KEYWORDS EST.
 SOURCE Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman, Ph.D.
 ORGANISM house mouse.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1. (bases 1 to 937)
 TITLE NIH-MGC http://mgi.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman, Ph.D.
 cDNA Library Preparation: ResGen, Invitrogen Corp
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM13885 row: f column: 18
 High quality sequence stop: 741.
 Location/Qualifiers
 1. 937

/organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:6393617"
 /clone_lib="NIH_MGC_130"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: oocytes; Vector: pCMV-SPORT6.1.ccd; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.95 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH MGC library."
 BASE COUNT 261 a 222 c 242 g 205 t 7 others
 ORIGIN

Query Match 16.6%; Score 336.2; DB 14; Length 937;
 Best Local Similarity 74.7%; Pred. No. 9.1e-62;
 Matches 422; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

Qy 583 GAATCCACCCCGCTCTTGAATACTGAAGCTGCTCACAGCTACACCCGAAAGATTT 642
 Db 292 GAGCCTCACCGGTTTGGAGAACTTCGGTCCATTAATACTATAACCTTAAAGATTT 351

Qy 643 GAGTGGAAATCTGAAAAGCGGCGTGTTCATCATCAAGAGCTACTCTGAGGACGATC 702
 Db 352 GACTGGAAATCTGAAAACATGCGCGGTTTTTCATCATTAAGAGCTACTCTGAGGACGATC 411

Qy 703 CACCGCTCCATTAAGTACTCCATCTGTTGATGACACAGACGCGCAACAGCGCTTGGAC 762
 Db 412 CACCGTTCCATTAAGTATAATATCTGTTGACGACACAGCATGGTACAGAGACTGGAT 471

Qy 763 AGCCCTTCGCTGATGAGACGAGGCGCGTCTACCTGCTCTTCAGCGTCAATGGG 822
 Db 472 GCCCCTATCGTTCCATGAATGGAGGGTCCCGTGTACTTTTCAGTGTCAAGCGC 531

Qy 823 AGTGGGCATTTTGTGGGGTGGCGGAGTGAAGTCCCGTGGACTACGACAGCGTCC 882
 Db 532 AGTGGACATTTCTGTGGAGTTGCAGATGAATCTCTGTGGACTACACACATGTGCA 591

Qy 883 GGGGTCTGGTCTCAGGACAAAGTGGAGGGGAAGTTTCATGTCCAGTGGATTTTGTAAAG 942
 Db 592 GGTGTGGTCCCGAGGACAAATGGAAGGGTCTTTCATGTCCAGTGGATTTTGTGAAG 651

Qy 943 GATGTACCCAAATACAGCTCCGACATCAGGCTGGAGAAATACGACACAAACCGGTC 1002
 Db 652 GACGTTCCCAATAGCCAACTCGCACACATTCGCTAGAGAAACACGAGATTAACCCAGTG 711

Qy 1003 ACAAACTCCCGGACACCCAGGAGTCCCTTAGAAAAGCCAGCAAGTCTGAAAATT 1062
 Db 712 ACCAACTCTAGGACATCTAGGAGTCCCTCTGGAAGAGCTAGCAGGTTTGAATAATC 771

Qy 1063 ATCAGTTCTTACAAGCACACAACTCCATCTTCGACGACTTTGCTACTACGAGAACGC 1122
 Db 772 ATAGCCAGCTACAAGCACACCACTTCCATTTTGTGATGACTTTCACACTATGAGAAACGC 831

Qy 1123 CAGAGGAGGAGGAGTGGTGGCGAA 1147
 Db 832 CAAGAGGGAAGAAGAGTGTAA 856

RESULT 88
 BQ63156
 LOCUS
 DEFINITION BQ63156 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL070e20 5', mRNA sequence.

ACCESSION BQ63156
 VERSION BQ63156.1 GI:17422181
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus.
 1 (bases 1 to 719)
 REFERENCE
 AUTHORS Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara

TITLE JOURNAL COMMENT	Expressed genes in X. laevis embryo Unpublished (2001) Contact: Tadao Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.
FEATURES source	Location/Qualifiers 1..719 /organism="Xenopus laevis" /db_xref="taxon:8355" /clone="XL070e20" /clone_lib="NIBB Mochii normalized Xenopus tailbud library" /tissue_type="whole embryo" /dev_stage="stage 25" /note="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, and (Wellcome/CRC Institute)."
BASE COUNT ORIGIN	230 a 135 c 157 g 196 t 1 others Query Match 16.6%; Score 336; DB 13; Length 719; Best Local Similarity 71.2%; Pred. No. 1e-61; Matches 472; Conservative 0; Mismatches 186; Indels 5; Gaps 2;
QY	568 TCTGCCCCCAGCGTCGAATCCACCCCGTCTTTGAAAACTGAAGGCTGTCTACAGCTAC 627
DB	14 TTTGCCTTCCTGTTGAAGTGACCCAGTACTGGAGAACTGAAGCCATTAACTAC 73
QY	628 AACCCGAAGAGTTTGAGTGGAACTCTGAAGCGGGCGTGTTCATCATCAGAGCTAC 687
DB	74 AATCCCAAGAGCTTTGACTGGAGTCTAAAAAATGGACAGTGTATTATTAAGAGCTAC 133
QY	688 TCTGAGGACGACATCCACCGCTCCATTAACTACTCCATCTGGTGTAGCAGAGCAGCGC 747
DB	134 TCTGAAGACCATATTCTATCGTTCTATAAAGTACTCAATCTGGTGTAGCAGCCGACATGGC 193
QY	748 AACAGCGCTGGACAGCGCTTCGCTGATGAGCAGCAGCAAGGGCGGCTCTACCTGCTC 807
DB	194 AATAAGCTTTGATGCTGCTTACCGATCTTTGAATGAAAGGCCACCTTTATTACTC 253
QY	808 TTGAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCCGAGATGAAGTCCCGCTGGAC 867
DB	254 TTCAGTGTAAATGGAAGTGGACATTTTGTGGTGTAGCTGAATGAAGTCTGTTGTGGAC 313
QY	868 TAGGGACCAAGTCCGGGTCGTGCTCAGGACAAAGTGAAGGGAGTTTGATGCCAG 927
DB	314 TATAATGCTTATGCTGGAGTCTGGTCCGAGCAATGGAAGGGAAGTTGATGTAATA 373
QY	928 TGGATTTTGTGAAGATGTACCAATAACACAGCTCCGGCACATCAGGCTGGAGATAAC 987
DB	374 TGGGCTTTGTCGAAGACGTACCTAATAACAGTTGGCGCATATTCGTTAGAAATAAC 433
QY	988 GACAACAAACCGGTACAAATCTCCGGGACACCCGAGAGGTGCGCTTAGAAAAAGCCAA 1047
DB	434 GATAACAAGCCTGTTACCAACTCAAGGACACCTCAAGAGGTTCCTCCCTAGAAAAAGGCC 493
QY	1048 CAAGTCTGAATATTACGTTCTTACAGCAGACACACCTCCATCTTCGACGACTTGGCT 1107
DB	494 CAAGTTCTTAAAAATAATGCAATGTTCAAGCATACAACCTCTATCTTTGATGACTTTGCA 553
QY	1108 CACTACAGAA--GCGCCAGAGGAGGAGGTGGTGCAGCAAGGAAACGGCAGAGTCGAAA 1165
DB	554 CATTATGAGNAGCGTCAAGGGGAGGAGCCATCGGTAGGGA---GCGAATCGAAA 610
QY	1166 CAACAATAGGGCGCAACGAGTTTCTTTACATGTTTCTAACGTTTGTGACTTTTGAAACAGTTT 1225

Db

611 CAACAATAATCTCGAGCGATATCTCTGTATTAATCACAACACTAATGATGTAGACTCTGG 670

QY

1226 AAA 1228
|||

Db

671 AAA 673
|||

RESULT 89

BE026361

LOCUS

DEFINITION

db37f12.v1 Blackshear/Soares normalized Xenopus egg library Xenopus laevis cDNA clone IMAGE:3300719 5', similar to TR:064556 O64556 YU8H12R.13 PROTEIN. ; mRNA sequence.

ACCESSION

BE026361

VERSION

BE026361.1

KEYWORDS

EST.

SOURCE

African clawed frog.

ORGANISM

Xenopus laevis

REFERENCE

1 (bases 1 to 632)

AUTHORS

Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wyllie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.

TITLE

WashU Xenopus EST project, 1999

JOURNAL

Unpublished (1999)

COMMENT

Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Bento Soares and M. Fatima Bonaldo (University of Iowa). DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 456.
Location/Qualifiers
1..632
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:3300719"
/clone_lib="Blackshear/Soares normalized Xenopus egg library"
/sex="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"

BASE COUNT

160 a 188 c 162 g 121 t 1 others

ORIGIN

Query Match 16.5%; Score 335.6; DB 10; Length 632;
Best Local Similarity 75.4%; Pred. No. 1.3e-61;
Matches 432; Conservative 0; Mismatches 135; Indels 6; Gaps 1;

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Qy 406 CCTCTCCAGCAGACGCCCGCCAGCTTTGGCTCAACGGCAGTATCAGAGCCCTCAGCAGCCA 465
Db 66 CCGCGCTGTCTAGACTCAATACCAAAATCCACGGCCCTCAACAGCAGCCACGACC 125
Qy 466 CCCAGACCCGCTGGTTGGCCCGCCAGCAACAGAACGGGGTTTGGGACAGCGGAGGG 525
Db 126 CCTCAGATCCGCTGGTGGCCCGCCAGGATAGGAACGCTGCTTATGGTCAGGGTGGAGGC 185
Qy 526 GCTGGCAGCAGTAGCAACTCTCTCGGAAACGTCAGCAGCCTAAATCTGCCCCCAGCGTCGAA 585
Db 186 CCA-----GATGGAAACCTCTGGAGGAGCCAGTCTCAGCTGCCCCCGGAAATGAG 239
Qy 586 TCCACCCCGCTCTGAAAAAAGCTGCTCAGAGCTCAGAGTACAGCCGAAAGAGTTTGAG 645
Db 240 TCTCACCCCTGTCTAGAGAAACTGAAAGCCGCCACAGCTACAAACCCCAAGGACTTTGAC 299
Qy 646 TGGAACTCTGAAAGCGGCGGTGTTCATCATCAAGAGCTACTCTGAGGAGCAGATCCAC 705
Db 300 TGGAACTCTGAAAGCGGCGGTGTTCATCAATAAAGAGCTACTCTGAGGATGATATCCAC 359
Qy 706 CGCTCCATTAAAGTACTCCATCTGTGTGTAGCAGACGCAACAGCGCCTGGACAGC 765
Db 360 GCTTCCATCAATACTCCATCTGTGTGACGACAGAGCATGGGAATAAAGCTTGGATAAC 419
Qy 766 GCCTTCGCTCAGCAGCAGCAAGGGGCCGCTCTACCTGCTCTTCAGCGTCAATGGAGT 825
Db 420 GCTTTCGCTCCATCAATATGGAAGCGCCGCTCTACCTTCTGTTCAGCGTCAACGGCAGT 479
Qy 826 GGGCATTTTGTGGGGTGGCGAGATGAAGTCCCGGAGTACGACAGCAGGCGCGGG 885
Db 480 GGACACTTTTTCGGGGTGGCGAGATGAAGTCCCGGAGTATGGCACCAGTGGCGGT 539
Qy 886 GTCTGGTCTCAGGACAAGTGGAAAGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGAT 945
Db 540 GTCTGGTCAAGGACAATGAAGGCAAGTTCAGCTCAAGTGGCTTTGTCAAGGAC 599
Qy 946 GTACCCCAATACAGGCTCCGCGACATCAGGCTG 978
Db 600 GTTGCCAAACACGCTGAGGCACATCGCCTG 632

RESULT 90
BQ232423
LOCUS
DEFINITION BQ232423 873 bp mRNA linear EST 02-MAY-2002
5', mRNA sequence.
AGENCOURT 7561139 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6054830
ACCESSION BQ232423
VERSION BQ232423.1 GI:20413823
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 873)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: ATCC/DCTP/DRP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13314 row: b column: 15
High quality sequence stop: 715.
FEATURES
"source", 1..873
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6054830"
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/clone_lib="NIH_MGC_72"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT 251 a 207 c 220 g 195 t
ORIGIN
Query Match 16.5%; Score 335.2; DB 14; Length 873;
Best Local Similarity 67.6%; Pred. No. 1.5e-61;
Matches 488; Conservative 0; Mismatches 228; Indels 6; Gaps 1;
Qy 416 CACAGCCCCAGCTTTGGCTCAACCGCAGTATCAGAGCCCTCAGCAGCCACCCAGACCC 475
Db 105 CTCACCTCCACACAGCCTGCCAGCTTTCAGTCCAGCAACAGGACGCTCAGCAACCC 164
Qy 476 GCTGGGTTGCCACGCAACAGAAACCGGCGGTTTGGGACAGCGGAGGCGCTGGCAGCG 535
Db 165 GCTGGGTAGCACCTCGGAACCGGTGGCAGTGGGTTCCGTCATAATGGGGTGGATGTAATG 224
Qy 536 ATACCAACTCTCTGGAAACGTCACAGCCTAAATCTGCCCCCAGCGTCGAATCCCAACCCCG 595
Db 225 GAGTAGACAGTCTCAGGCTGGTTCGGATCTACTCTTC-----AGAACCCCAACCCAG 278
Qy 596 TCCTTGA AAAAATGAAAGGCTGCTCACAGCTACAAACCCGAAAGAGTTTGAAGTGAATCTGA 655
Db 279 TGTGGAGAGCTTCGGTCCATTAATAACTATAACCCCAAGATTTTGAAGTGAATCTGA 338
Qy 656 AAACGGCGGTGGTTTCATCATCAAGAGCTACTCTGAGGACGACATCCACGCTCCATTA 715
Db 339 AACATGCGCGGTTTTCATCATTAAGAGCTACTCTGAGGACGATATTCACCGTTCCATTA 398
Qy 716 AGTACTCCATCTGTGTAGCAGACGACGCAACAGCGCTGGACAGCGCTTCCGCT 775
Db 399 AGTATAATATTTGTGTGACGACAGAGCATGTGTAAAGAGACTGGATGCTGCTTATCGTT 458
Qy 776 GCATGACAGCAAGGGGCCGCTCTACCTGCTCTTACCGCTCAATGGGAGTGGGCAATTTT 835
Db 459 CCATGAACGGGAAAGGCCCGTTTACTTTTCACTGTCAACGGCAGTGGACACTTCT 518
Qy 836 GTGGGTGGCGGAGATGAAGTCCCGCTGAGCTACGGCAGCAGTCCCGGGGTCTGGTCTC 895
Db 519 GTGGCGTGGCAGAAATGAAATCTGCTGGAGTACAAACATGTGACAGTGTGTGGTCCC 578
Qy 896 AGGACAAAGTGGAGGGGAAGTTTGATGTCCAGTGGATTTTGTGTAAGGATGTACCCAAATA 955
Db 579 AGGACAAATGGAAGGGTGGTTTGTATGTAGTGGATTTTGTGNAAGGACGTTCCCAATA 638
Qy 956 ACCAGCTCCGGCAGCATCAGGCTGGAGAAATAACGACAAACCCGGTCACAAACTCCCGGG 1015
Db 639 GCCAACTGCGACACATTCGCTAGAGAAACAGAGAAATAAACAGTGCACCACTCTAGGG 698
Qy 1016 ACACCCAGGAGTGGCCCTTAGAAAAAGCCAGAGCTGCTGAAAAATTTATCAGTTCCTACA 1075
Db 699 ACACCTAGGAAGTGGCTCTCGAAAAAGGCTAAGCAGAGTGTGAAAAATTTATAGCCAGCTACA 758
Qy 1076 AGCACAAACCTCCATCTTCGAGACTTTTCTCAGAGAGAGCGCCAGAGAGGAGGA 1135
Db 759 AGCACACACTTCCATTTTGTATGACTTCTCACACTATGAGAAACGCCCAAGAGAGAAAGA 818
Qy 1136 GG 1137
Db 819 AG 820

RESULT 91
H69270
LOCUS
DEFINITION H69270 363 bp mRNA linear EST 13-AUG-1996
ACCESSION H69270
VERSION H69270.1 GI:1030687
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KEYWORDS EST. human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 363)
AUTHORS Jay, P.
TITLE Human cDNAs from HEGW library
JOURNAL Unpublished (1995)
COMMENT Other ESTs: T90361
Contact: Jay, P.
Centre de Recherches de Biochimie Macromoléculaire
Centre National de Recherches Scientifiques (CNRS)
1919 route de Mende, 34033 Montpellier, France
Tel: 3367613349
Fax: 3367521559
Email: pj@merlin.crbm.cnrs-mop.fr
Seq primer: T3.
FEATURES
source
1..363
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20p11"
/clone="HEGWCRI15"
/note="Vector: lambda zap; Site 1: EcoRI; Site 2: XhoI; using an oligodT-XhoI primer. After second strand synthesis, an EcoRI adaptor was ligated and the cDNA was size selected on an agarose gel before directional cloning in the EcoRI and XhoI sites of lambda Zap vector."
BASE COUNT 111 a 83 c 95 g 70 t 4 others
ORIGIN
Query Match 16.4%; Score 333.4; DB 14; Length 363;
Best Local Similarity 98.1%; Pred. No. 48-61; Mismatches 5; Indels 2; Gaps 2;
Matches 356; Conservative 0;
QY 873 CACCAGTGC CGGGGTCTGGTCTCAGGACAAAGTGGAAAGGGAAGTTTGATGTC CAGTGGAT 932
DB 1 CACCAGTGC CGGGGTCTGGTCTCAGTCAAGTGGAAAGGGAAGTTTGATGTC CAGTGGAT 60
QY 933 TTTTGTAAAGGATGATACCAATACCAGTCCGGCACATCAGGCTGGAGATTAACGACAA 992
DB 61 TTTTGTAAAGGATGATACCAATACCAGTCCGGCACATCAGGCTGGAGATTAACGACAA 120
QY 993 CAACCGGTGACAACTCCGGGACACCCAGGAGTGCCCTTAGAAACCCCAAGCAAGT 1052
DB 121 CAACCGGTGACAACTCCGGGACACCCAGGAGTGCCCTTAGAAACCCCAAGCAAGT 180
QY 1053 GCTGAAATTTATCAGTTCTTACAGACACCACTCCATCTTCGACGACTTTTGCTCACTA 1112
DB 181 GCTGAAATTTATCAGTTCTTACAGACACCACTCCATCTTCGACGACTTTTGCTCACTA 240
QY 1113 CGAAGACGCGCA - GAGGAGGAGGAGTGTGCGCAAGGAAACGACAGTCCGAAACAA 1171
DB 241 CGAAGACGCGCAAGGAGGAGGAGTGTGCGCAAGGAAACGACAGTCCGAAACAA 300
QY 1172 ATGAGGCGAACAGTTCTTACATGTTCTTAAGTTTGACTTT - GAACAGTTTAAAC 1230
DB 301 ATGAGGCGAACAGTTCTTACATGTTCTTAAGTTTGACTTTTGAGAAACAGTTTAAAC 360
QY 1231 ACG 1233
DB 361 ACG 363
RESULT 92
BO989797 943 bp mRNA linear EST 16-AUG-2002
LOCUS AGENCOURT_8749084 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6334535
DEFINITION 5', mRNA sequence.
ACCESSION BO989797
VERSION BO989797.1 GI:22291811

KEYWORDS EST. house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 943)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman, Ph.D.
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM13795 row: h column: 24
High quality sequence start: 21
High quality sequence stop: 530.
FEATURES
source
1..943
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:6334535"
/lab_host="NIH MGC 130"
/lab_host="DH10B (phage-resistant)"
/note="Organ: otcysts; Vector: pCMV-SPORT6.1.cdb; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.95 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH MGC Library."
BASE COUNT 173 a 305 c 265 g 199 t 1 others
ORIGIN
Query Match 16.4%; Score 333.4; DB 14; Length 943;
Best Local Similarity 86.6%; Pred. No. 3.6e-61; Mismatches 367; Conservative 0; Indels 0; Gaps 0;
QY 1 CAAAGGACAAGATAATAAGTACAAATGGTTCGTATCATCAGAGGATACAGTTTCATG 60
DB 228 CAAAGGACAAGATAATAAGTACAAATGGTTCGTATCATCAGAGGATACAGTTTCATG 287
QY 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGAGTAAACAGTACCCCTCAA 120
DB 288 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGAGTAAACAGTACCCCTCGA 347
QY 121 TGAGGACACCCCTACCTGTCCAGCTATTACCGCGCTCCATTGGATTTCCTTACTCCCTCA 180
DB 348 TGAGTGATCTTTACCTGTCCAGTTACTATCCACCATCCATTGGATTTCCTTACTCCCTCA 407
QY 181 ATGAGGCTCGGTGTTACTTGAGGGGACCTCCGATTCCTACCTCACCACCTACGGAC 240
DB 408 GCAGGACCATGTGTCCACTGCGAGGGGACCTCCCATCCCGTATCTCATTACCTATGGAC 467
QY 241 AGCTCAGTAACGAGACCATCATTTTATGCAGATGCTGTTTTGGGACGCTCGGGGGCC 300
DB 468 AACTTAGTAATGGAGACCATCACTTCATGATGATGCTGTTTTGGGACGCTCGGGGTC 527
QY 301 TGGGGAACAACATCTATCAGCACAGTTTCAATTTTTTCCCTGAAAAACCCCTGCGTTCTCAG 360
DB 528 TGGGGAACAACCTTTTACCAGCACAGTTTAAATTTTTTCCCTGAAAAACCCCTGCGATTCTCAG 587
QY 361 CATGGGGACAAGTGGGTCTCAAGGTTCAGAGACCCAGAGCTCAGGCTCTCCAGCACAG 420
DB 588 CATGGGGGACCGTGGTTCTTCAGGGGACGAGACTCAGAGCTCAGGCTATGGAGGAGTT 647
QY 421 CCCC 424
DB 648 ACCC 651

```

RESULT 93
AA636479
LOCUS
DEFINITION
v18d03.r1 Barstead mouse myotubes MFLRB5 Mus musculus cDNA clone
IMAGE:1120997.5, mRNA sequence.
ACCESSION
AA636479
VERSION
AA636479.1 GI:2560258
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 542)
Marra, M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B.,
Theising, B., Wylie, F., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:610333
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 512.
Location/Qualifiers
1..542
/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:1120997"
/clone_lib="Barstead mouse myotubes MFLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
/notes="vector: p77T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACCAATCGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AAATCGGATCCITG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified p77T3 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(availible from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."
BASE COUNT 131 a 152 c 134 g 125 t
ORIGIN
Query Match 16.4%; Score 333; DB 9; Length 542;
Best Local Similarity 89.0%; Pred. No. 4,7e-61;
Matches 371; Conservative 0; Mismatches 45; Indels 1; Gaps 1;
Qy 1 CAAAGGCAAGATAATAAGTACAAAATGGTTCGTATCATCAGAAGGATACAGTTTCATG 60
Db 116 CAAAGGCAAGATAATAAGTACAAAATGGTTCGTATCATCAGAAGGATACAGTTTCATG 175
Qy 61 ACATGACTTTGAGCCCTACCTTACTGACAGTCAATCAGTACAGTTACCCCTCA 120
Db 176 ACAATGACTTTGAGCCCTACCTTCTTGACAGTCAATCCGAGTAACTACCCCTCGA 235
Qy 121 TGAGGACCCCTACCTGTCACAGTATTATCCCGCCCGTCCATGGATTCTCTACTCCCTCA 180
Db 236 TGAGTGATCCCTTACCTGTCCAGTTACTTACCACTCACTGATTTCTTACTCCCTCA 295
Qy 181 ATGAGGCTCGGTGTCCTACTGCGAGGGGACCCCTCCGATTCCATACCTACCCACCTACGGAC 240

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Db 296 GCGAGGCACCATGGTCCACTTCAGGGGA-CCTCCCATCCCGTATCTCACTACCTATGGAC 354
Qy 241 AGCTCAGTAACGAGACCATCATTTTATGACAGTGTCTGTTTTTGGGAGAGCTGGGGGCC 300
Db 355 AACTTAGTAATGGAGACCATCATCTTCATGATGATGCTGTTTTTGGGAGAGCTGGGGGTC 414
Qy 301 TGGGGAACAACATCTATCAGCACAGGTTCAATTTTTTCCCTGAAACACCTCGGTTCTCAG 360
Db 415 TGGGGAACAACATTTACCAGCACAGGTTTAATTTTTTCCCTGAAACACCTCGATTTCTCAG 474
Qy 361 CATGGGGACAAGTGGGTCTCAAGGTGACGAGCCAGCTCAGCTCAGCTCTCCCAGCA 417
Db 475 CATGGGGACAAGTGGGTCTCAGGGGACGAGCTCAGCTCAGCTTATGGGAGCA 531

RESULT 94
BM772351
LOCUS
DEFINITION K-EST0056477 S4SNU1s1 Homo sapiens cDNA clone S4SNU1s1-1-B07 5',
mRNA sequence.
ACCESSION
BM772351
VERSION
BM772351.1 GI:19101966
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 694)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoseun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr
Place: 1 row: B column: 07
High quality sequence stop: 694.
Location/Qualifiers
1..694
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S4SNU1s1-1-B07"
/clone_lib="S4SNU1s1"
/sex="M"
/tissue_type="Stomach"
/cell_type="Lymphoblast-like"
/lab_host="Top10F"
/notes="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
inact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Burg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
sequencing about 2,000 ~ 3,000 colonies in original cDNA
library, the abundant cDNAs were selected and amplified by
PCR reaction using vector region primer including T7

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promotor as 5' primer and Nid14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells *E. coli* Top10F⁺ with electroporation method."

BASE COUNT 162 a 222 c 189 g 120 t 1 others
ORIGIN

Query Match 16.4%; Score 333; DB 14; Length 694;
Best Local Similarity 100.0%; Pred. No. 4.6e-61;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 400 GCTCAGCCTCTCCAGCAGACCCCGCTTTGGCTCAACCGAGTATCAGACCCCTCAG 459

DB 362 GCTCAGCCTCTCCAGCAGACCCCGCTTTGGCTCAACCGAGTATCAGACCCCTCAG 421

QY 460 CAGCCACCCAGACCCCGCTTTGGCTCAACCGAGTATCAGACCCCTCAG 519

DB 422 CAGCCACCCAGACCCCGCTTTGGCTCAACCGAGTATCAGACCCCTCAG 481

QY 520 GAGGGGCTGGCAGCAGTACCACTCTCTGGAAGCTCCAGCCTAATTCTGCCCCAGC 579

DB 482 GAGGGGCTGGCAGCAGTACCACTCTCTGGAAGCTCCAGCCTAATTCTGCCCCAGC 541

QY 580 GTCGAATCCACCCCGCTTTGAAAACCTGAAGCTGCTCAGAGTACACCCGGAAGAG 639

DB 542 GTCGAATCCACCCCGCTTTGAAAACCTGAAGCTGCTCAGAGTACACCCGGAAGAG 601

QY 640 TTTGAGTGAATCTGAAAGCGGCTGCTTCATCATCAAGAGTACTCTGAGGAGCAG 699

DB 602 TTTGAGTGAATCTGAAAGCGGCTGCTTCATCATCAAGAGTACTCTGAGGAGCAG 661

QY 700 ATCCACCGCTCCATTAAAGTACTCCATCTGGTG 732

DB 662 ATCCACCGCTCCATTAAAGTACTCCATCTGGTG 694

RESULT 95
BM748094 505 bp mRNA linear EST 04-MAR-2002
LOCUS X-EST0022789 SSSNU484 Homo sapiens cDNA clone SSSNU484-20-G06 5',
DEFINITION mRNA sequence.
ACCESSION BM748094
VERSION BM748094.1 GI:19077712
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 505)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yusong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 20 row: G column: 06
High quality sequence stop: 505.
Location/Qualifiers
1. 505
/organism="Homo sapiens"
/db_xref="taxon:9606"

FEATURES
source

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/clone_lib="SSSNU484"
/sex="M"
/tissue_type="Stomach"
/cell_type="Epithelial"
/cell_line="SNU-484"
/lab_host="Top10F"

/note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was decapped with tobacco
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
including EcoRI site by treatment of T4 RNA ligase. The
first strand cDNA was synthesized from oligo dT-selected
mRNA by priming with dT-tailed vector. The dT-tailed
vector was adjusted to have about 60nt. The cDNA vector
was circularized with *E. coli* DNA ligase after digestion
of EcoRI which site is also included in vector. An RNA
strand converted to a DNA strand by Okayama-Berg method.
The obtained cDNA vectors were used for transformation of
competent cells *E. coli* Top10F⁺ by electroporation
method."

BASE COUNT 124 a 171 c 129 g 81 t
ORIGIN

Query Match 16.4%; Score 332; DB 14; Length 505;

Best Local Similarity 100.0%; Pred. No. 7.7e-61;

Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 400 GCTCAGCCTCTCCAGCAGACCCCGCTTTGGCTCAACCGAGTATCAGACCCCTCAG 459

DB 174 GCTCAGCCTCTCCAGCAGACCCCGCTTTGGCTCAACCGAGTATCAGACCCCTCAG 233

QY 460 CAGCCACCCAGACCCCGCTTTGGCTCAACCGAGTATCAGACCCCTCAG 519

DB 234 CAGCCACCCAGACCCCGCTTTGGCTCAACCGAGTATCAGACCCCTCAG 293

QY 520 GAGGGGCTGGCAGCAGTACCACTCTCTGGAAGCTCCAGCCTAATTCTGCCCCAGC 579

DB 294 GAGGGGCTGGCAGCAGTACCACTCTCTGGAAGCTCCAGCCTAATTCTGCCCCAGC 353

QY 580 GTCGAATCCACCCCGCTTTGAAAACCTGAAGCTGCTCAGAGTACACCCGGAAGAG 639

DB 354 GTCGAATCCACCCCGCTTTGAAAACCTGAAGCTGCTCAGAGTACACCCGGAAGAG 413

QY 640 TTTGAGTGAATCTGAAAGCGGCTGCTTCATCATCAAGAGTACTCTGAGGAGCAG 699

DB 414 TTTGAGTGAATCTGAAAGCGGCTGCTTCATCATCAAGAGTACTCTGAGGAGCAG 473

QY 700 ATCCACCGCTCCATTAAAGTACTCCATCTGGTG 731

DB 474 ATCCACCGCTCCATTAAAGTACTCCATCTGGTG 505

RESULT 96

AA361068

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 341)

Adams,M.D., Karlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

,C.J., Lee,N.H., Kirkness,E.F., Weinschick,K.G., Gocayne,J.D., White

,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,

Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodok,A.,

Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,

Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,

Moreno-Palanco,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

AA361068 341 bp mRNA linear EST 21-APR-1997
EST70314 T-cell lymphoma Homo sapiens cDNA 5' end, mRNA sequence.

AA361068

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 341)

Adams,M.D., Karlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

,C.J., Lee,N.H., Kirkness,E.F., Weinschick,K.G., Gocayne,J.D., White

,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,

Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodok,A.,

Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,

Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,

Moreno-Palanco,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

Other ESTs: THCI92215

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1. 341

/organism="Homo sapiens"

/db_xref="ATCC (inhost):165217"

/db_xref="taxon:9608"

/clone_lib="T-cell lymphoma"

/cell_type="T-lymphocyte"

/note="Vector: pbluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 91 a 80 c 86 g 82 t 2 others

ORIGIN

Query Match 16.1%; Score 327; DB 9; Length 341;

Best Local Similarity 99.1%; Pred. No. 9.4e-60;

Matches 338; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 991 AACAAACCGGTACAAACTCCGGGACACCCAGGAGTGCCTTAGAAAAAGCCAGCAA 1050

|||||

Db 1 AACAAACCGGTACAAACTCCGGGACACCCAGGAGTGCCTTAGAAAAAGCCAGCAA 60

|||||

QY 1051 GTGCTGAAATTTATCAGTTCTTACAAGCACACCACTCCATCTTCGACGACTTTGCTCAC 1110

|||||

Db 61 GTNCTGAAATTTATCAGTTCTTACAAGCACACCACTCCATCTTCGACGACTTTGCTCAC 120

|||||

QY 1111 TACGAGAGCCCA-GAGGAGGAGGAGTGTGCGCAAGGACGAGAGTGCAGAACAAA 1169

|||||

Db 121 TACGAGAGCCCAAGGAGGAGGAGTGTGCGCAAGGACGAGAGTGCAGAACAAA 180

|||||

QY 1170 CAATGAGGGCAACAGTTTCTTACATGTTCTTACAGTTTGAATTTGAAACAGTTTAAAA 1229

|||||

Db 181 CAATGAGGGCAACAGTTTCTTACATGTTCTTACAGTTTGAATTTGAAACAGTTTAAAA 240

|||||

QY 1230 CACGTGTCTTGTGTGTCAGTGTGTCGTCGCGGGGGTGTGAGTGTGTCATCTTT 1289

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Db 241 CACGTGTCTTGTGTGTCAGTGTGTCGTCGCGGGGGTGTGAGTGTGTCATCTTT 300

|||||

QY 1290 GCCTTTCTTGTGTTGTTTGGCCAGATGGATCTGCATT 1330

|||||

Db 301 GCCTTTCTTGTGTTGTTTGGCCAGATGGATCTGCATT 341

|||||

RESULT 97

AW465429

LOCUS

BP230019A20A9 Soares normalized bovine placenta Bos taurus CDNA

DEFINITION clone BP230019A20A9 5', mRNA sequence.

ACCESSION AW465429

VERSION AW465429.1 GI:7035597

KEYWORDS

SOURCE

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS

Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson

J.H.

Bovine ESTs

Unpublished (2000)

Contact: Lewin, H. A.

W. M. Keck Center for Comparative and Functional Genomics

University of Illinois at Urbana-Champaign

340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL

61801, USA

Tel: 217 333 5998

Fax: 217 244 5617

Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.

PCR Primers

FORWARD: TAATAGACTCACTATAGGG

BACKWARD: ATTAACCTCACTAAAG

Insert Length: 530 Std Error: 0.00

Plate: BP230019A20 row: A column: 9

Seq primer: AGCGATAACAATTTACACAGGA

High quality sequence stop: 530.

Location/Qualifiers

1. 530

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="Soares normalized bovine placenta"

/sex="Female"

/lab_host="DH10B"

/notes="Organ: Placenta; Vector: p7T3pac; Site_1: EcoRI;
Site_2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."

BASE COUNT 154 a 122 c 126 g 128 t

ORIGIN

Query Match 16.1%; Score 326.8; DB 10; Length 530;

Best Local Similarity 76.0%; Pred. No. 1e-59;

Matches 403; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 594 CGTCTTGAATAACTGAAGGCTGCTCACAGCTACACCCGAAAGATTGTAGTGGATCT 653

Db 1 CGTCTTGAAGAAGTTCGGTCCATTAACTATAACCCCAAGGATTTTGACTGGAAATCT 60

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QY 654 GAAAGCGGGCGTGTTCATCAACAAGAGTACTCTGAGGACACATCCACCGCTCCAT 713

|||||

Db 61 GAAACATGGCGGGTTTTCATTAAGAGCTACTCCGAGGACGATATCCACCGTTCAT 120

|||||

QY 714 TAAGTACTCCATCTGGTGTAGCAGACGAGCGCAAGCGCTGGACAGCGCTCCG 773

|||||

Db 121 TAAGTATAATATCTGGTGCAGCAGAGCATGGTAAACAGAGACTGGATGCTGTATCG 180

|||||

QY 774 CTGCATGAGCAGCAAGGGCGGCTGCTACCTGCTCTTCAGCGTCAATGGAGTGGCATTT 833

|||||

Db 181 CTCCATGAACGGGAAGCGCCCGCTTTTACTTTTTCAGTGTCAACGGCAGTGGACACTT 240

|||||

QY 834 TTGTGGGGTGGCCGAGATGAAGTCCCGCTGGACTACGGACACAGTGCCTGGGCTGTC 893

|||||

Db 241 CTGTGTGTGCGAGAAATGAATCTGTGTGGACTACACACATGTGCGAGTGTGTGTC 300

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QY 894 TCAGGACAAAGTGGGAAGGGGAAGTTTGTATGTCACATGGATTTTGTAAAGATGTACCCAA 953

|||||

```
*
Db 301 CAGGACAAATGAAGGCGCGTTTGTGATGTCAAGTGGATTTTTGTGAAGACGTTCCCAA 360
QY 954 TAAACCACTCCGACATCAGCGTGGAGATAACGACAAACAAACCGGTCAACAACTCCCG 1013
Db 361 TAGCCAACCTGGACATTCGCCCTAGAGACACAGGAGATAAACCACTAGCAACTCCAG 420
QY 1014 GACACCCAGGAGTGCCTTTAGAAAAAGCAAGAGCTGCTGAAATATATCATGTTCTTA 1073
Db 421 GGACACTCAGGAAGTGCCTCTGAAAAAGCTAAGCAGGTGTTGAAATCATATGCCAGCTA 480
QY 1074 CAGACACAACTCCATCTTCACGACTTGTCTCACTACGAGAGCGCC 1123
Db 481 CAAGCACACCACTTCCATTTTGTATGACTTCTCACACTATGAGAAAGCGCC 530

RESULT 98
LOCUS N95559 411 bp mRNA linear EST 09-APR-1996
DEFINITION yy60d10.r1 Soares_multiple_sclerosis_2NbHMSF Homo sapiens cDNA
clone IMAGE:277939 5', mRNA sequence.
ACCESSION N95559
VERSION N95559.1 GI:1267868
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 411)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,D., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston
,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ETPRimer
High quality sequence stop: 374.

FEATURES
source
1..411
/organism="Homo sapiens"
/db_xref="GDB:3896315"
/db_xref="taxon:9606"
/clone="IMAGE:277939"
/clone_lib="Soares_multiple_sclerosis_2NbHMSF"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: pT73D (Pharmacia) with a modified
polylinker V type: phagemid; Site 1: Not I; Site 2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dr)
primer [5'
TGTACCAATCTGAATGGAGCGCGCATTTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis
lesions from one patient was kindly provided by Dr. Kevin
G. Becker (NINDS/NIH)."
BASE COUNT 107 a 102 c 116 g 82 t 4 others
ORIGIN
```

Query Match 16.0%; Score 324.8; DB 14; Length 411;
Best Local Similarity 95.2%; Pred. No. 2.7e-59;

```
Matches 377; Conservative 0; Mismatches 14; Indels 5; Gaps 4;
QY 652 CTGAAAAGCGGCGGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGACATCCACCGCTCC 711
Db 1 CTGAAAAGCGGCGGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGACATCCACCGCTCC 60
QY 712 ATTAAGTACTTCATCTGGTGTAGCACAGAGCGGCAACAAAGCGCTTGACACGCGCTTC 771
Db 61 ATTAAGTACTTCATCTGGTGTAGCACAGAGCGGCAACAAAGCGCTTGACACGCGCTTC 120
QY 772 CGCTGATCAGCAGCAAGGCGCGCTCTACCTGCTCTTCAGCGTCAATGGAGTGGGCAT 831
Db 121 CGTGTATGAGCA -CAAGGGGCGCGCTCTACCTGCTCTTCAGCGTCAATGGAGTGGGCAT 179
QY 832 TTTTGTGGGTGGCGGAGATGAAGTCCCGCTGGACTACGGCACCGAGTGCGGGGTCTGG 891
Db 180 TTTTGTGGGTGGCGGAGATGAAGTCCCGCTGGACTACGGCACCGAGTG -CGGGGTCTGG 238
QY 892 TCTCAGGACAAGTGGAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGGATGTACCC 951
Db 239 TCTCAGGACAAGTGGAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGGATGTA -CC 297
QY 952 AATAACCAAGTCCGGCACATCAGGCTGGAGATAACGACAAACACCGGTCACAAACTCC 1011
Db 298 AATAACCAAGTCCGGCACATCAGGCTGGAGATAACGACAAACACCGGNCACAAACTCC 357
QY 1012 CGGGCACCCAGGAGTGGCGCTTAGAAAAAGCCAAG 1047
Db 358 -GGGACACCAAGAGGTGCTTAGAAAAAGCAANAAG 391

RESULT 99
LOCUS BG499817 695 bp mRNA linear EST 27-MAR-2001
DEFINITION 602545252F1 NTH_MGC_60 Homo sapiens cDNA clone IMAGE:4667581 5',
mRNA sequence.
ACCESSION BG499817
VERSION BG499817.1 GI:13461334
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 695)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1476 row: h column: 14
High quality sequence stop: 691.

FEATURES
source
1..695
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4667581"
/clone_lib="NIH MGC 60"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: prostate; Vector: pDNR-Lib (Clontech);
Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggccattggcc
); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCCATTATGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGCGGCGGCACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
```

insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

```
BASE COUNT      211 a  151 c  168 g  165 t
ORIGIN
Query Match      16.0%; Score 323.6; DB 12; Length 695;
Best Local Similarity 76.0%; Pred. No. 4.7e-59;
Matches 413; Conservative 0; Mismatches 129; Indels 1; Gaps 1;
Qy 583 GAATCCCAACCCCGTCTTGAAGAGCTGCTCAGCTACAAACCGAAGAGTTT 642
Db 33 GAACCCCAACCCAGTGTGGAGAGCTTCGGTCCATTAATACTATAACCCCAAGATTTT 92
Qy 643 GAGTGGAACTGAAAGCGGCGGTGTTCATCATCAAGACTACTCTGAGAGACATC 702
Db 93 GACTGGAATCTGAAACATGCGCGGGTTTTTCATCAATTAAGAGCTACTCTGAGGACGATAT 152
Qy 703 CACCGCTCCATTAAAGTACTCCATCTGTGTAGCAGACGCGCAACAACGCGCTGGAC 762
Db 153 CACCGTCCATTAAAGTAAATATTTGGTGCAGCAGAGCATGGTAACAAGAGACTGGAT 212
Qy 763 AGCGCTTTCGCTGCTGATGAGCAAGGGGCCGCTCTACCTGCTCTTTCAGCGTCAATGGG 822
Db 213 GCTGCTTATCGTTCATGAACGGAAGGCCCGCTTTACTTTTACAGTGTCAACGGC 272
Qy 823 AGTGGGCAATTTTGTGGGTGGCGAGATGAAGTCCCCCGTGGAGCTAGCGGCACGAGTGC 882
Db 273 AGTGGACACATTTCTGTGGCGTGGCAGAAATGAATCTGCTGTGGACTACAAACACATGTGA 332
Qy 883 GGGGTCTGTCTCAGGACAACTGGAAGGGGAAGTTTGATGTCAGTGGATTTTGTGAAG 942
Db 333 GGTGTGTGTCCTCCAGGCAAAATGAAGGGTC-GTTTGTATGTAGTGGATTTTGTGAAG 391
Qy 943 GATGTACCCAAATAACAGCTCCGACATCAGGCTGGAGAAATAACGAAACCAACCGGTC 1002
Db 392 GACGTTCCTAATAGCAACTCGGACACATTCGCTAGAGAACACGAGAAATAAACCAAGT 451
Qy 1003 ACAAACTCCCGGGACACCCAGGAGGTGCCCTTAGAAAAGCAAGCAAGCTGCTGAAATTT 1062
Db 452 ACCAACTCTAGGACACTCAGGAAGTGCCTCTGGAAGAGGCTTAAGCAGGTGTTGAAATTT 511
Qy 1063 ATCAGTTCTTACAGCACACAACTCCATCTTCCGACGACTTTGCTCACTACGAGAGCGC 1122
Db 512 ATGCCAGCTACAGCACACCACTTCCATTTTGTATGACTTCTCACACTATGAGAAACGC 571
Qy 1123 CA 1124
Db 572 CA 573
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RESULT 100
LOCUS      AL774891
DEFINITION AL774891 XGC-gastrula Silurana tropicalis cDNA clone TGas080113 5',
            mRNA sequence.
ACCESSION  AL774891
VERSION    AL774891.1 GI:21560595
KEYWORDS   EST.
SOURCE     western clawed frog.
ORGANISM   Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
            Xenopodinae; Silurana.
REFERENCE  1 (bases 1 to 654)
AUTHORS   Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.
TITLE     Sanger Xenopus tropicalis EST project 2002
JOURNAL   Unpublished (2001)
COMMENT   Contact: Taylor R
            Sanger Centre
            Hinxton, Cambridgeshire, CB10 1SA, UK
```

Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TGas080113.plkSP6
Sequencing primer: PlkSP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.

FEATURES

Location/Qualifiers

1..654

/organism="Silurana tropicalis"

/db_xref="taxon:8364"

/clone="TGas080113"

/clone_lib="XGC-gastrula"

/dev_stage="gastrula (stages 10.5-13 mixed)"

/lab_host="Escherichia coli XL1-blue"

/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA

was oligo dT primed from 5' end of poly A+ RNA from stages

10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated

into pCS107 with EcoRI at the 5' end and NotI at the 3'

end."

BASE COUNT 152 a 229 c 175 g 98 t

ORIGIN

Query Match 15.9%; Score 322.4; DB 9; Length 654;
Best Local Similarity 80.9%; Pred. No. 8.6e-59;
Matches 390; Conservative 0; Mismatches 86; Indels 6; Gaps 1;

Qy 436 CAACCGCAGTATCAGAGCCCTCAGCAGCACCCAGACCGCTGGTGGCCACGCAAC 495

Db 179 CCACCGCCCTCAGCAGCAGCCACAGGCCCTCAGAACCGCTGGTGGCCACGCAAC 238

Qy 496 AGAAACCGCGGTTTGGGCGAGCGGAGGGCTGGCGCGATAGCAACTCTCTGGAAAC 555

Db 239 AGGAACGCTGCTTACGCCAGGGCGGA-----GGCCCGGACGGGAACCTCTCGGGCGG 292

Qy 556 GTCAGGCTAATTTGCGCCCGCAGCGTCGAATCCACCCCGCTCTTGAAGAACTGAAGCT 615

Db 293 GCTCAGTCTCCTCCGCGCCCTGGGAACGAGTCCACCCCGCTGCTGGAGAACTGAAGGCC 352

Qy 616 GTCACAGCTACAAACCGAAAGAGTTTGTAGTGAATCTGAAAGCGGCGCTGTTCATC 675

Db 353 GCCCAGAGCTACAAACCCAGAGCTTTGACTGGAACTTGAAGAAACGGGCGCTGTTCATA 412

Qy 676 ATCAAGAGCTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCTCATCTGCTGTAGC 735

Db 413 ATAAAGAGCTACTCCGAGGACGACATCCACCGCTCCATCAAGTACTCCATCTGCTGCAGC 472

Qy 736 ACAGAGCAGGCAACAGCGCTGGACAGCGCTTCCGCTGCATGAGCAGCAAGGGGCC 795

Db 473 ACAGAGCAGGCAACAGCGCTGGATAGCGCTTCCGCTCCATGAACGGCAAGGGGCC 532

Qy 796 GTCTACCTGTCTTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCGAGATGAAG 855

Db 533 GTCTACCTTCTGTTTCAGCGTCAACGGCAGGGGACATTTCTGCGCGTGGCCGAGATGAAG 592

Qy 856 TCCCGCGTGGACTACGGCACAGTGGCGGGCTGTGGTCTCAGGACAAAGTGAAGGGGAAG 915

Db 593 TCCCGCGTGGACTACGGCACAGTGGCGGGCTGTGGTCTCAGGACAAAGTGAAGGGGAAG 652

Qy 916 TT 917

Db 653 TT 654

Search completed: March 24, 2003, 01:13:56

Job time : 3534 secs

Mon Mar 24 15:50:03 2003

T., Waterston, R. and Wilson, R.
Washu-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 831 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 436.
Location/Qualifiers

FEATURES
source

1. .447
/organism="Homo sapiens"
/db_xref="GDB:5924646"
/db_xref="taxon:9606"
/clone="IMAGE:727735"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
Inc., and primed with a Not I - oligo(dT) primer [5].
TGTTACCACTCTGAAGTGGGCGGCGCCCAATTTTCTTTTCTTTT 3].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 103 a 75 c 111 g 158 t
ORIGIN
Query Match 13.5%; Score 274; DB 1; Length 447;
Best Local Similarity 100.0%; Pred. No. 3.7e-59;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1755 TTGAAATCTTTCTTCAGATCTTTGCCCACTGAAAGCAGCCCGCTCCCTCACTGTC 1814
Db 1 TTGAAATCTTTCTTCAGATCTTTGCCCACTGAAAGCAGCCCGCTCCCTCACTGTC 60
1815 CTGGTCTCGATGGCTGGTGGTGGGCGATGATGTGGAGGAATCGAAGGTGC 1874
61 CTGGTCTCGATGGCTGGTGGTGGGCGATGATGTGGAGGAATCGAAGGTGC 120
QY 1875 TTTAGTCTGGTTTCAGGTTCGGGCGATCTTTTGTGTTGTCACATCTTTTAAATTTTACA 1934
Db 121 TTTAGTCTGGTTTCAGGTTCGGGCGATCTTTTGTGTTGTCACATCTTTTAAATTTTACA 180
QY 1935 CCTTTCTTAAGAAATCTTAATCCGCTCTTAAGTTTATACCAATATGCTGAGCTTTAA 1994
Db 181 CCTTTCTTAAGAAATCTTAATCCGCTCTTAAGTTTATACCAATATGCTGAGCTTTAA 240
QY 1995 GTGAGGATCTGGTAGTACACAGATGTGATGA 2028
Db 241 GTGAGGATCTGGTAGTACACAGATGTGATGA 274

RESULT 68
AW641341 553 bp mRNA linear EST 26-APR-2001
LOCUS
DEFINITION
cn06d01.w1 Blackshear/Soares normalized xenopus egg library Xenopus
laevis cDNA clone PBX0105D01 5', mRNA sequence.
ACCESSION
AW641341.1 GI:7398599
VERSION
KEYWORDS
EST.
SOURCE
African clawed frog.
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoides; Pipidae;

REFERENCE
AUTHORS

TITLE
JOURNAL
MEDLINE
COMMENT

Xenopodinae; Xenopus.
1 (bases 1 to 553)
Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G.
Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman
J.W., Bonaldo, M.F., and Soares, M.B.
The NIHES Xenopus maternal EST project: interim analysis of the
first 13,879 ESTs from unfertilized eggs
Gene 267 (1), 71-87 (2001)
21211403
Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
USA
Tel: 919 541-4899
Fax: 919 541-4571
Email: black009@niehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
cdna@resgen.com
DNA Sequencing and analyses performed by National Institutes of
Health Intramural Sequencing Center (NISC).
PCR Primers
FORWARD: TGTAAAACGACGGCCAGT
BACKWARD: CAGGAACAGCTATGACC
Plate: 0105 row: D column: 01
Seq primer: T7 primer.
Location/Qualifiers

FEATURES
source

1. 553
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="PBX0105D01"
/clone_lib="Blackshear/Soares normalized Xenopus egg
library"
/sex="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
/note="Vector: pT73-Pac; Site 1: EcoRI; Site 2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
pT73-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subtraction: two
approaches to facilitate gene discovery', Genome Research
6:791-806, 1996. The first strand synthesis used a
NotI-dT18 primer; double stranded cDNAs were ligated to
EcoRI adapters, digested with NotI, and directionally
cloned into the NotI and EcoRI-digested pT73-Pac vector.
The library contained approximately 7.2 X 10⁵
recombinants, with average insert sizes of 1-1.5 kb."
BASE COUNT 139 a 155 c 125 g 134 t

BASE COUNT
ORIGIN

Query Match 13.5%; Score 273; DB 2; Length 553;
Best Local Similarity 78.4%; Pred. No. 7e-59;
Matches 327; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 1 CAAAGGACAGATATATAAGTACAAATGTTGTTTACATCAGAAGGATACAGTTCTATG 60
Db 33 CAAACAAATGATCTTATTTTCAGTTTCAAAACGATCCCTGTCATCAGAAGGACAGGTGCAGC 92
QY 61 ACAATGATTTTGACCTTACCTTACTGACAGTCAATCAGAGTAAACAGTTACCCCTCAA 120
Db 93 ATAATGATTTTGACAGTACCTGTGCGGGGAGTCCATCAGATTAACAGTACCCCTTCCA 152
QY 121 TGAGCGACCCCTTACTGTCTCCAGCTATTACCCCGGTTCATTTGGATTTCCTTACTCCCTCA 180
Db 153 TGACAGACCCCTTACTATCCAGTTACTACCTCTCTTATTTGGTTTCGGTATTCCTCTCA 212
QY 181 ATGAGGCTCCGTGGTCTACTGTCAGGGGACCTTCGATTTCCATACCTCACCACCTACGGAC 240

/clone_lib="NCI_CGAP GC4"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from 3 pooled
 germ cell tumors, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pRT3
 vector. Library is normalized. Library was constructed by
 Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 169 a 162 c 133 g 215 t

Query Match 14.0%; Score 284; DB 1; Length 679;
 Best Local Similarity 74.0%; Pred. No. 1.2e-61;
 Matches 37; Conservative 0; Mismatches 130; Indels 1; Gaps 1;
 QY 670 TTATCATCAAGAGCTACTCTGAGGACGACATCCACCGCTCCATTAAGTATCTCATCTGG 729
 Db 679 TTATCATTAAGAGCTACTCTGGGACGATATTTACCGTTCCATTAAGTATTAATTTGG 620
 QY 730 TGTAGCAGAGCAGCGCAACAGCGCTTGACAGCGCTTCCGCTGCATGACGAGCAAG 789
 Db 619 TGCAGCAGGAGCATGTTAACAAGAGACTGCTGCTTATCGTTTCATGAACGGGA 560
 QY 790 GGGCCCTCTACCTCTCTTCAGGCTCAATGGGAGTGGGCTTTTGTGGGGTGGCCGAG 849
 Db 559 GGGCCCGTTTACTTACTTTTTCAGTGTCAACGGCAGTGGACACTTCTGTGGCGTGGCAGAA 500
 QY 850 ATGAAGTCCCGGTGGACTACGGCAGCAGTCCCGGGTCTGCTCTCAGGCAAGTGAAG 909
 Db 499 ATGAAATCTGCTGGACTACACACATGTGCGAGTGTGGTCCCGAGCAATGGAAG 440
 QY 910 GGAAGTTTTCATGCTCAGTGGATTTTGTAAAGATGTACCATTAACAGCTCCGCGAC 969
 Db 439 GGTGCTTTTGTATGCTCAGTGGATTTTGTGAGACGTTTCCCATAGCAACTGGGACAC 380
 QY 970 ATCAGCTGAGATACGACCAACACCGGTCAAACTCCCGGGACACCCAGGAGGTG 1029
 Db 379 ATTGGCTAGAGAACACGAGATAAACAGTACCAACTCTAGGAGACACTCAGGAAGTG 320
 QY 1030 CCCTTAGAAAAGCCAGCAAGTGTGTAATTTATCATGTTCTTACAGGACACCACTCC 1089
 Db 319 CCTCTGAAAAGGCTAAGCAGGTGTGTAATTTATAGCCAGCTACAGGACACCACTTC 260
 QY 1090 ATCTTCGACGACTTGTCTACTACGAGAGCGCC-AGAGGAGGAGGAGTGTGCGCAG 1148
 Db 259 ATTTTGTATGACTTCTCACACTATGAGAACGCGCAAGAGAGAGAAAGTGTTTAAAG 200
 QY 1149 GAACGCAAGTCAAAACAA 1172
 Db 199 GAACGTCAGGTGCGGGAATAA 176

RESULT 66
 AL627746
 LOCUS AL627746 XGC-gastrula 689 bp mRNA linear EST 02-NOV-2001
 DEFINITION AL627746 XGC-gastrula Silurana tropicalis cDNA clone TGAs025h05 5',
 mRNA sequence.
 ACCESSION AL627746
 VERSION AL627746.1 GI:16597229
 KEYWORDS EST.
 SOURCE western clawed frog.
 ORGANISM Silurana tropicalis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 Xenopodinae; Silurana.
 1 (bases 1 to 689)
 Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
 Sanger Xenopus tropicalis EST project 2001 (10_2001)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Huckle E

FEATURES
 source
 1. 689
 Location/Qualifiers
 /organism="Silurana tropicalis"
 /db_xref="taxon:8364"
 /clone="TGAs025h05"
 /clone_lib="XGC-gastrula"
 /dev_stage="gastrula (stages 10.5-13 mixed)"
 /lab_host="Echerichia coli XL1-blue"
 /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
 was oligo dT primed from sug of poly A+ RNA from stages
 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
 into pCS107 with EcoRI at the 5' end and NotI at the 3'
 end."

BASE COUNT 139 a 253 c 166 g 129 t 2 others
 ORIGIN
 Query Match 13.6%; Score 274.8; DB 1; Length 689;
 Best Local Similarity 79.4%; Pred. No. 2.6e-59;
 Matches 324; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
 QY 1 CAAAGGACAAAGATAAAGTACAAAATGGTTGTTACATCAGAGGATACAGTTTCATG 60
 Db 243 CAAACAATGATCTTATTTTCAGTTCAAAACGGATCCCTGCACCAAGAGGACAGCGTGCCAG 302
 QY 61 ACATGACTTTGAGCCCTACCTTACTTGGACAGTCAAAATCAGAGTAACAGTTTACCCCTCAA 120
 Db 303 ATATGACTTCGAGCAGTACCTGTGGGACAGTCCCAATCAGAGTACAGCTACCCCTCCA 362
 QY 121 TGAGCACCCCTAGCTGTCCAGCTATTACCGCGCTTCATTCGATTCCTTACTCCCTCA 180
 Db 363 TGACGACCCGCTACCTGTCCAGTTACTACCTCTCTTATCGGCTTTCCGTATTCGCTCA 422
 QY 181 ATGAGCTCCGTGGTCTACTGCGAGGGAGCCCTCCGATTCCATACCTCACCACCTAGGAC 240
 Db 423 GCGAGCTCTTGGTCAACGGCGGGGACCCCGCATCCGTAACCTCCCGTACGGAC 482
 QY 241 AGCTGATGACGGAGACCATCAATTTTATGCAGATGCTGTTTTGGGAGCCTTGGGGGCC 300
 Db 483 AGCTGAGCAACGGAGACCAACCAATTTTCATGCAGATGCGTCTTTGGGAGCCTGGGGGCC 542
 QY 301 TGGGGAACAACATCTATCAGCACAGTTCATTTTTTCTCTGAAAACCTCGGTTCTCAG 360
 Db 543 TGGGAATAACATCTATCAGCACCGGTTCACTTCTCCCGGAAAACCCAGCCTTTTCG 602
 QY 361 CATGGGGGACAAAGTGGGTCTCAAGGTGACGAGACCCAGAGCTCAGCCT 408
 Db 603 CATGGGGGACGAGCGGCTCCGANGGAGCAGACCCAGAGCTCCGCT 650

RESULT 67
 AA398704
 LOCUS AA398704 447 bp mRNA linear EST 12-AUG-1997
 DEFINITION zt70h04.01 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727735
 3', mRNA sequence.
 ACCESSION AA398704
 VERSION AA398704.1 GI:2051817
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 447)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, P., Theising, B., White, Y., Wyllie

REFERENCE
 AUTHORS
 HILLIER, L., ALLEN, M., BOWLES, L., DUBUQUE, T., GEISEL, G., JOST, S.,
 KUCABA, T., LACY, M., LE, N., LENNON, G., MARRA, M., MARTIN, J., MOORE, B.,
 SCHELLENBERG, K., SEPTOE, M., TAN, P., THEISING, B., WHITE, Y., WYLLIE

CULT 87
9696
US

DEFINITION BO899696 mRNA linear EST 16-AUG-2002
AGENCOURT 8753787 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6393617
S' mRNA sequence.

ACCESSION BO899696
VERSION BQ899696.1 GI:22291698
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1..(bases 1 to 937)
NTH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
Ph.D.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: Agencourt Bioscience Corporation
Distribution: MGC clone distribution information can be
obtained through the I.M.A.G.E. Consortium/LLNL at:
mga@llnl.gov
EST reference stop: 741.
Qualifiers

Db	652	GACGTTCCCAATAGGCAACTGGCACACATGCTTAGAGAACACGAGATATACCACTG	711
Qy	1003	ACAAATCTCCCGGACACACCAGAGAGTGCCCTTAGAAAAAGCCAAAGTGTGAAAAAT	1062
Db	712	ACCACTCTTAGGACACTCAGGAGTGCTCTGGAAAAAGCTAAGCAGGTGTGAAAAATC	771
Qy	1063	ATCAGTTCCTACAAGCACACAACTCCATCTTCGAGGACTTGTGCATCTACGAGAACGC	1122
Db	772	ATAGCCAGCTACAAGCACACCACTCCATTTTTTGATGACTTCTCACATATGAGAAACGC	831
Qy	1123	CAGAGGNGGAGGTGGTGGCCAA	1147
Db	832	CAAGAGGAAGAAGTGTTTAA	856

RESULT	88
BJ063156	
LOCUS	719 bp mRNA linear EST 07-DEC-2000
DEFINITION	BJ063156 NTBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL070620 5', mRNA sequence.
ACCESSION	BJ063156
VERSION	BJ063156.1 GI:17422181
KEYWORDS	EST.
SOURCE	African clawed frog.
ORGANISM	Xenopus laevis
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus.
AUTHORS	1 (bases 1 to 719) Kitayama, A., Terasaka, C., Mochii, M., Veno, N., Shin-i, T. and Kohara

```

ORIGIN

Query Match          16.7%; Score 338; DB 9; Length 917;
Best Local Similarity 88.8%; Pred. No. 3.8e-62;
Matches 366; Conservative 17; Mismatches 27; Indels 2; Gaps

QY 1 CAAAAGGACAGAATAATAAGTACAAAATGGTTGGTTACATCAGAAGGATACAGATTCATG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 278 CAAAAGGACAAATAATAATWTTTACAAAATGGTTGGTTACATCATATAGGWTATATTTCA 337
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 ACAATGACTTTGAGCCCTACCTTACTTGGACAGTCAAATCAGAGTAACAGTATACCCCTCAA 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 338 AYAATTAYTTTTAKCYCTACCTTACTTGGACATTTAAATVAGATTTACATTTACCCCTYAA 397
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 TGAGCAGACCCCTACCTGTGTCAGCTATTATCCGCGGTCATTGGATTTCTTACTCCCTCA 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 398 TTAGCTACCCCTACCTTTTCAGCTATTATTCGCTTTTATTTGGAATTCCTTACTCCCTCA 457
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 181 ATCAGAGCTCCGGT-GTCTACTCGAGGGGACCTCCGATTCCTCATCTACCACTTACGGA 239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 458 ATGAGGCTCCGGTGTGTATTTCGTGGKTAACCTCCGATTCCTCATCTACCACTTACGGA 517
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 240 CAGCTCAGTAAACGAGACCATCATTTTATGACAGCATGCTGTTTTTGGGAGAGCTCGGGG 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 518 CAGCTCAGTAAACGAGAGCCATCATTTATGACAGATGCTGTTTTTGGGAGAGCTCGGGG 577
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 300 CTGGGAAACAATCTATCAGCACAGGTTCAAATTTTTTCCCTGAAAAACCTCGGTTCTCA 359
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 578 CTGGGAAACAATCTATCAGCACAGGTTCAAATTTTTTCCCTGAAAAACCTCGGTTCTCA 637
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 360 GCAT-GGGGGACAAGTGGGTCTCAAGGTCAGAGTACGAGACCGAGCTCAGCCTCT 410
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 638 GCATGGGGGACAAGTGGGTCTCAAGGTCAGAGTACGAGACCGAGCTCAGCCTCT 699
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 86
AA460050
LOCUS
DEFINITION
355 bp mRNA linear EST 09-JUN-1997
zx65c02.r1 Soares total fetus Nb2HP8_9w Homo sapiens cDNA clone
IMAGE:796418.5, similar to TR:G849195 G849195 CHROMOSOME IV COSMID
9481.; mRNA sequence.
ACCESSION
AA460050
VERSION
AA460050.1 GI:2184934
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 355)
AUTHORS
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Stepcoe, M., Tan, F., Theising, B., White, Y., Wyllie,
T., Waterston, R., and Wilson, R.
TITLE
WashU-Merck EST Project 1997
JOURNAL
Unpublished (1997)
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 325.
Location/Qualifiers
1..355
/organism="Homo sapiens"
/db_xref="GDB:6040577"
/db_xref="taxon:9606"
/clone="IMAGE:796418"
/clone_lib="Soares total_fetus_Nb2HP8_9w"
/dev_stage="8-9 weeks"

COUNT	174 a	274 c	228 g	206 t	35 others
http://fulllength.invitrogen.com					

REFERENCE 1 (bases 1 to 732)

AUTHORS Buerstedde, J.M.
 TITLE Gallus gallus bursal lymphocyte EST
 JOURNAL Unpublished (2002)
 COMMENT Contact: Buerstedde JM
 Cellular Immunology
 Heinrich-Pette-Institute
 Martinistr. 52, 20251 Hamburg, Germany
 Email: URL: http://genetics.bpi.uni-hamburg.de/dt40est.html.
 Location/Qualifiers
 1..732

FEATURES

source
 1..732
 /organism="Gallus gallus"
 /db_xref="taxon:9031"
 /clone="3502r1"
 /clone_lib="rikeni"
 /cell_type="bursal lymphocyte"
 /dev_stage="2-3 weeks old"
 /note="CB inbred strain"
 201 a 173 c 168 g 190 t

BASE COUNT

ORIGIN
 Query Match 14.9%; Score 301.8; DB 1; Length 732;
 Best Local Similarity 82.7%; Pred. No. 3.5e-66;
 Matches 345; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

1 CAAAGGACAGATATAAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 60
 Db 100 CGAAGGACAGATATAAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCACG 159
 Qy 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAAAATCAGAGTAAACAGTTACCCCTCAA 120
 Db 160 ACAACGATTTTGAACCTTACCTTTCTGGGAGTCAAAATCAGAGTAAACAGTTACCCCTCAA 219
 Qy 121 TGACGACCCCTACTGTCAGCTATTTACCGCGGTCAATTTGATTTCTTACTCCCTCA 180
 Db 220 TGACTGATCCTTATCTGTCAGTATTATTCACCATCTATCGGGTTTCCCTACTCTCA 279
 Qy 181 ATGAGGCTCGGTGCTACTGACGGACCTCGATTCATCTCAGATCCTACACACCTACCGAC 240
 Db 280 GTGAAGCGGCATGCTTACAGGAGGATCTCTATCCCGTATCTCACCACCTATGGAC 339
 Qy 241 AGCTAGTACGGAGACCATCATTTTATGACAGATGCTGTTTTGGGACCTCGGGGCC 300
 Db 340 AGCTAGTATGAGATCATTTTATGATGATGCTGTTTTGGGACCTCGGGGCC 399
 Qy 301 TGGGGACACATCTATCAGACAGTTCAATTTTTCCTGAAACCTCGGCTCTCAG 360
 Db 400 TGGGAATATATCTATCAACACCGGTTTAACTTTTCCCTGAAATCTCGCTCTCAG 459
 Qy 361 CATGGGGCAAGTGGTCTCAAGTCCAGGACAGGACCTCAGCTCCTCCAGCA 417
 Db 460 CTTGGGACACAGTGGATCCCAAGGACAGGACTCAAAAGTTCCAGCATATGGGAGCA 516

RESULT 56

AA099707
 LOCUS
 DEFINITION zk96a12.r1 Soares pregnant uterus_NbHPu Homo sapiens CDNA clone
 IMAGE:489694 5', mRNA sequence.
 AA099707
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 EST.
 human.
 AA099707 421 bp mRNA linear EST 11-MAY-1997

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 421)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Wards, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.

REFERENCE

AUTHORS

LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 RESULT 57
 AJ397688
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 AJ397688
 741 bp
 mRNA
 linear
 EST 25-JAN-2001
 dkEz426 Gallus gallus CDNA clone 30j10r1, mRNA sequence.

TITLE

JOURNAL

MEDLINE

COMMENT

Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 97044478

Contact: Wilson RK

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: esc@watson.wustl.edu

This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 811 Std Error: 0.00
 Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 360.

FEATURES

source

1..421
 /organism="Homo sapiens"
 /db_xref="GDB:3804281"
 /db_xref="taxon:9606"
 /clone="IMAGE:489694"
 /clone_lib="Soares_pregnant_uterus_NbHPu"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: pT73-Pac; Site 1: Not 1;
 Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer [5',
 AACTGGAAGATTCGGCGCGCTTTTTCATTTTTCAGACAC-3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization. Library
 constructed by M. Fatima Bonaldo." 4 others
 97 a 70 c 94 g 156 t

BASE COUNT

ORIGIN

Query Match 14.8%; Score 300.4; DB 1; Length 421;
 Best Local Similarity 98.2%; Pred. No. 6.9e-66;
 Matches 323; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
 Qy 1700 CTGCTAGACAGATACTTTTAAATTTTCAAAATTCAGACACATTTTTCATTTTTCGA 1759
 Db 1 CTGCTAGACAGATACTTTTAAATTTTCAAAATTCAGACAC-3' 59
 Qy 1760 AATCTTTCTTCCAGATCTGTTGCCACTGAAACCCACCGTCCCTCACTGCTCGT 1819
 Db 60 AATCTTNCCTTCCAGATCTGTTGCCACTGAAACCCACCGTCCCTCACTGCTCGT 119
 Qy 1820 GTCCGATTTGGGCTGGATGTTGGGCGCATGATGTGGAGGAACTGKAGGTCCTTAG 1879
 Db 120 GTCCGATTTGGGCTGGATGTTGGGCGCATGATGTGGAGGAACTGKAGGTCCTTAG 179
 Qy 1880 GTCTGTTTCAGGCTGGGCTTTTGTGTTGTCACATCTTTTAAATTTTACACCTTT 1939
 Db 180 GTCTGTTTCAGGCTGGGCTTTTGTGTTGTCACATCTTTTAAATTTTACACCTTT 239
 Qy 1940 TCTTAAGAATTTCAATGCGCTTAAAGTTTATACCAATATGCTGAGCTTTAAGTGT- 1998
 Db 240 TCTTAAGAATTTCAATGCGCTTAAAGTTTATACCAATATGCTGAGCTTTAAGTGT- 299
 Qy 1999 AGGATCTGTTAGTACAGACAGTGTGATGG 2027
 Db 300 AGGATCTGTTAGTACAGACAGTGTGATGG 328

RESULT 57

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

promotor as 5' primer and N(dt)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA probes by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the substracted cDNA libraries were constructed by transfection of the remaining DNA into competent cells E. coli Top10F. with electroporation method."

ASE COUNT 162 a 222 c 189 g 120 t 1 others
 Query Match 16.4%; Score 333; DB 14; Length 694;
 Best Local Similarity 100.0%; Pred. No. 4.6e-61;
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 400 GGTGAGCTCTCCAGCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 459
 b 362 GGTGAGCTCTCCAGCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 421
 Y CAGCCACCCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 519
 b 422 CAGCCACCCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 481
 Y 520 GGAGGGCTGGGAGGATAGCACTCTCTGGAAACGTCAGGCTTAATCTGCCCCCAGC 579
 b 482 GGAGGGCTGGGAGGATAGCACTCTCTGGAAACGTCAGGCTTAATCTGCCCCCAGC 541
 Y 580 GTGGAATCCACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 639
 b 542 GTGGAATCCACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 601
 Y 640 TTTGAGTGAATCTGAAAGCGGGCGTGTCTCATCATCAGAGCTACTCTGAGGAGCAG 699
 b 602 TTTGAGTGAATCTGAAAGCGGGCGTGTCTCATCATCAGAGCTACTCTGAGGAGCAG 661
 Y 700 ATCCACCGCTCCATTAAGTACTCATCTCGTGT 732
 b 662 ATCCACCGCTCCATTAAGTACTCATCTCGTGT 694

RESULT 95
 M748094 505 bp mRNA linear EST 04-MAR-2002
 OCUS X-EST0022789 S5SNU484 Homo sapiens cDNA clone S5SNU484-20-G06 5',
 EFinition mRNA sequence.
 CCESSION BM748094.1 GI:19077712
 ERSION BM748094
 OURC human.
 ORGNISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 505)
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 20 row: G column: 06
 High quality sequence stop: 505.
 Location/Qualifiers
 1..505
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

/clone="S5SNU484-20-G06"
 /clone.lib="S5SNU484"
 /sex="M"
 /tissue_type="Stomach"
 /cell_type="Epithelial"
 /cell_lines="SNU-484"
 /lab_host="Top10F"

/note="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was decapped with tobacco
 acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
 including EcoRI site by treatment of T4 RNA ligase. The
 first strand cDNA was synthesized from oligo dt-selected
 mRNA by priming with dt-tailed vector. The dt-tailed
 vector was adjusted to have about 60nt. The cDNA vector
 was circularized with E. coli DNA ligase after digestion
 of EcoRI which site is also included in vector. An RNA
 strand converted to a DNA strand by Okayama-Berg method.
 The obtained cDNA vectors were used for transfection of
 competent cells E. coli Top10F by electroporation
 method."

BASE COUNT 124 a 171 c 129 g 81 t

Query Match 16.4%; Score 332; DB 14; Length 505;

Best Local Similarity 100.0%; Pred. No. 7.7e-61;

Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 400 GGTGAGCTCTCCAGCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 459

Db 174 GGTGAGCTCTCCAGCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 233

QY 460 CAGCCACCCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 519

Db 234 CAGCCACCCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 293

QY 520 GGAGGGCTGGGAGGATAGCACTCTCTGGAAACGTCAGGCTTAATCTGCCCCCAGC 579

Db 294 GGAGGGCTGGGAGGATAGCACTCTCTGGAAACGTCAGGCTTAATCTGCCCCCAGC 353

QY 580 GTGGAATCCACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 639

Db 354 GTGGAATCCACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 413

QY 640 TTTGAGTGAATCTGAAAGCGGGCGTGTCTCATCATCAGAGCTACTCTGAGGAGCAG 699

Db 414 TTTGAGTGAATCTGAAAGCGGGCGTGTCTCATCATCAGAGCTACTCTGAGGAGCAG 473

QY 700 ATCCACCGCTCCATTAAGTACTCATCTCGTGT 731

Db 474 ATCCACCGCTCCATTAAGTACTCATCTCGTGT 505

RESULT 96

AA361068

LOCUS

DEFINITION

AA361068.1

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 341)

Adams, M.D., Karlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White

, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,

Cline, T.R., Cotton, M.D., Barle-Hughes, J., Fine, L.D., Fitzgerald

, L.M., Fitzhugh, W.M., Pritchman, J.L., Geoghagen, N.S., Glodok, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,

Kelley, J.C., Liu, L.-I., Marra, S.M., Merrick, J.M., Moreno-Palancas, S.M.,

Moreno-Palancas, S.M., McDonald, L.A., Nguyen, D.T., Fellgrino, S.M.,

Phillips, C.A., Ryder, S.B., Scott, J.L., Saudak, D.M., Shirley, R.,

341 bp mRNA linear EST 21-APR-1997

T-cell lymphoma Homo sapiens cDNA 5' end, mRNA sequence.

Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P., and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert size: 957
High quality sequence stops: 381
Source: IMAGE Consortium, LUNL
This clone is available royalty-free through LUNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 957 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 381.

TITLE
JOURNAL
COMMENT

High quality sequence stops: 381
Source: IMAGE Consortium, LUNL
This clone is available royalty-free through LUNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 957 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 381.

High quality sequence stops: 381
Source: IMAGE Consortium, LUNL
This clone is available royalty-free through LUNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 957 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 381.

High quality sequence stops: 381
Source: IMAGE Consortium, LUNL
This clone is available royalty-free through LUNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 957 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 381.

High quality sequence stops: 381
Source: IMAGE Consortium, LUNL
This clone is available royalty-free through LUNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 957 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 381.

High quality sequence stops: 381
Source: IMAGE Consortium, LUNL
This clone is available royalty-free through LUNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 957 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 381.

High quality sequence stops: 381
Source: IMAGE Consortium, LUNL
This clone is available royalty-free through LUNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 957 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 381.

FEATURES
source

1. 629
/organism="Homo sapiens"
/db_xref="GDB:551383"
/db_xref="taxon:9606"
/clone="IMAGE:142344"
/clone_lib="Soares placenta Nb2HP"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pTV73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
AACTGGAAGATTCGGCGCGGAGGATTTTCTTTTCTTTT 3'),
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pTV73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 144 a 101 c 139 g 238 t 7 others
ORIGIN
Query Match 21.0%; Score 426; DB 14; Length 629;
Best Local Similarity 97.8%; Pred. No. 5.3e-81;
Matches 452; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

1568 GTCAATTAGAGTATCTCGATAAATCTCTTGAAATCTCAATCAAAAGGTTAATGTT 1627
11 GGCATTTAGAGTATCTCGATAAATCTCTTGAAATCTCAATCAAAAGGTTAATGTT 70
1628 TTTTGTCTATCTGATTTGTCATTTATCTGTTATCGTCTAAGTCTAATTTACC 1687
71 TTTTGTCTATCTGATTTGTCATTTATCTGTTATCGTCTAAGTCTAATTTACC 130
1688 CATTGATTTTCTGCTAGACAGATTAATTTTCAATTTTGGCAGACACTTTT 1747
131 CATTGATTTTCTGCTAGACAGATTAATTTTCAATTTTGGCAGACACTTTT 190
1748 TTTTGTCTATCTGATTTGTCATTTATCTGTTATCGTCTAAGTCTAATTTACC 1807
191 TTTTGTCTATCTGATTTGTCATTTATCTGTTATCGTCTAAGTCTAATTTACC 250
1808 CACTGTCTGCTGATTTGGGCTGATGTTGTTGGGCTGATGTTGGGCTGATGTT 1867
251 CACTGTCTGCTGATTTGGGCTGATGTTGTTGGGCTGATGTTGGGCTGATGTT 310
1867 CACTGTCTGCTGATTTGGGCTGATGTTGTTGGGCTGATGTTGGGCTGATGTT 1927
251 CACTGTCTGCTGATTTGGGCTGATGTTGTTGGGCTGATGTTGGGCTGATGTT 370
1927 CACTGTCTGCTGATTTGGGCTGATGTTGTTGGGCTGATGTTGGGCTGATGTT 1985
251 CACTGTCTGCTGATTTGGGCTGATGTTGTTGGGCTGATGTTGGGCTGATGTT 429
1985 CACTGTCTGCTGATTTGGGCTGATGTTGTTGGGCTGATGTTGGGCTGATGTT 2027

Db 430 GAGCTTTAAGTGTAGGATCNGGTAGTACAGACAGTGTGATGG 471

RESULT 48
BJ044639/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

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Query 100.0%; Pred. No. 4.6e-82;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

CAGCCTCTCCAGCAGCAGCCCGCTTGGCTCAACCGCAGTATCAGAGCCCTCAG 459
5 GCTCAGCTCTCCAGCAGCAGCCCGCTTGGCTCAACCGCAGTATCAGAGCCCTCAG 64
460 CAGCCACCCAGCAGCCCGCTTGGCTCAACCGCAGTATCAGAGCCCTCAG 519
65 CAGCCACCCAGCAGCCCGCTTGGCTCAACCGCAGTATCAGAGCCCTCAG 124
520 GGAGGGCTGGCAGGATAGCAACTCTCTGAAAGCTCAGCCTAATCTGCCCCAGC 579
125 GGAGGGCTGGCAGGATAGCAACTCTCTGAAAGCTCAGCCTAATCTGCCCCAGC 184
580 GTCGAATCCACCCCGCTCTGAAAGCTCAGGCTGCTCAGAGTACAAACCCGAAAG 639
185 GTCGAATCCACCCCGCTCTGAAAGCTCAGGCTGCTCAGAGTACAAACCCGAAAG 244
640 TTGAGTGGAAATCTGAAAGCGGGCTGTGTTCAATCAACAGAGTACTCTGAGGAC 699
245 TTGAGTGGAAATCTGAAAGCGGGCTGTGTTCAATCAACAGAGTACTCTGAGGAC 304
700 ATCCACCGCTCCATTAAGTATCTCCATCTGGTGTAGCAGAGCAGCAACAGGCGCTG 759
305 ATCCACCGCTCCATTAAGTATCTGGTGTAGCAGAGCAGCAACAGGCGCTG 364
760 GACAGCGCTTCCGCTGATCAGCAGCAGGCGGCTGCTACCTGCTTCCAGGCTCAAT 819
365 GACAGCGCTTCCGCTGATCAGCAGCAGGCGGCTGCTACCTGCTTCCAGGCTCAAT 424
820 GGGAGTGGGCA 830
425 GGGAGTGGGCA 435

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RESULT 46
LOCUS B1224711
DEFINITION 602949342F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:5093698 5',
mRNA sequence. EST 11-JUL-2001
ACCESSION B1224711
VERSION B1224711.1 GI:14678155
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLM1861 row: c column: 11
High quality sequence stop: 584.
Location/Qualifiers
1. 623

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5093698"
/clone_lib="NIH MGC"
/tissue type="Burkitt lymphoma"
/lab host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pORF7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dr priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 179 a 141 c 155 g 148 t

Query Match 21.2%; Score 430.8; DB 13; Length 623;
Best Local Similarity 89.5%; Pred. No. 4.9e-82;
Matches 54; Conservative 0; Mismatches 52; Indels 12; Gaps 7;

```

Qy 857 CCCCGGTGGACTACGGCACCAACCGGTCTGCTCAGGACAGAGTGGAGGGAAGT 916
Db 2 CCCCGGTGGACTACGGCACCAACCGGTCTGCTCAGGACAGAGTGGAGGGAAGT 61
Qy 917 TTGATGTCCAGTGGATTTTGTAAAGGATGTACCCCAATACCCAGTCCGGCAGCATCAGGC 976
Db 62 TTGATGTCCAGTGGATTTTGTAAAGGATGTACCCCAATACCCAGTCCGGCAGCATCAGGC 121
Qy 977 TGGAGATACGACCAACACCGGTCAAACTCCCGGACACCCAGAGGTGCCCTTAG 1036
Db 122 TGGAGATACGACCAACACCGGTCAAACTCCCGGACACCCAGAGGTGCCCTTAG 181
Qy 1037 AAAAGCCAAAGCAAGTGTGAAAATATCAGTTCCTACAGCAGCAGCAACCTCCATCTTCG 1096
Db 182 AAAAGCCAAAGCAAGTGTGAAAATATCAGTTCCTACAGCAGCAGCAACCTCCATCTTCG 241
Qy 1097 ACAGTTTGTCTACTACGAGAGCGCCA-CAGGAGGAGGAGGTGGTGGCAGAGCAAGCGGC 1155
Db 242 ACAGTTTGTCTACTACGAGAGCGCCA-CAGGAGGAGGAGGTGGTGGCAGAGCAAGCGGC 301
Qy 1156 AGAGTGGAAACAAACATGAGGGCGAACCAAGATTCTTAACATTGTGTAAAGTGGACT 1212
Db 302 AGAGTGGAAACAAACATGAGGGCGAACCAAGATTCTTAACATTGTGTAAAGTGGACT 361
Qy 1213 TTCAAAACAG-...TTTAAACACAGTGTGCTGTAGCTCCAG-TGTGTGTGCCCGTGGC 1268
Db 362 TGTGAAACAGTGTGCTGTAGCTCCAG-TGTGTGTGCCCGTGGC 421
Qy 1269 GGGGTTGA--GTGTTGCATCTTTGCCCTT-TCTGTGCTGTGAT-TTTTGGCCAGATGATC 1324
Db 422 GGGGTTGAGCTGTAGCATCTTTGCCCTTATCTGTGCTGTATATATGCCCAGATGATC 481
Qy 1325 TGCATTTATTGTACTTTTCTTTTATGATTAATCTCTAGAGTCACTAATAAAGAGT 1384
Db 482 TGCATTTATTGTACTTTTCTTTTATGATTAATCTCTAGAGTCACTAATAAAGAGT 541
Qy 1385 ATTTTTTTTTGTGCTTATCAATCAGACTGATCTAATGTGAAATGTAAAGTATCTTAA 1444
Db 542 CATACACCCGTCAGCTTATCAATCAGACTGATCTAATGTGAAATGTAAAGTATCTTAA 601
Qy 1445 AACAAAGC 1452
Db 602 CACACAC 609

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RESULT 47
R69898
LOCUS
DEFINITION Y147a01.r1 Soares placenta ND2HP Homo sapiens cDNA clone
IMAGE:142344 5', mRNA sequence.
ACCESSION R69898
VERSION R69898.1 GI:843415
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 629)
Hallier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman
M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J.,

R69898 629 bp mRNA linear EST 01-JUN-1995
Y147a01.r1 Soares placenta ND2HP Homo sapiens cDNA clone
IMAGE:142344 5', mRNA sequence.